



Docket No.: CL001188  
Serial No.: 09/817,198  
Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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1 TGCCCCGCTGC CCGCCCCGAG TTCCCGGCCC CGCTGGCCCC AGTCATGGCG
51 AAGCAGTACG ATGTGCTGTT CCGGCTGCTG CTGATCGGGG ACTCCGGGGT
101 GGGCAAGACC TGCCTGCTGT GCCGCTTCAC CGACAACGAG TTCCACTCCT
151 CGCACATCTC CACCATCGGT GTTGACTTTA AGATGAAGAC CATAGAGGTA
201 GACGGCATCA AAGTGCAGAT ACAGATCTGG GACACTGCAG GGCAGGAGAG
251 ATACCAGACC ATCACAAGC AGTACTATCG GCGGGCCCAG GGGATATTTT
301 TGGTCTATGA CATTAGCAGC GAGCGCTCTT ACCAGCACAT CATGAAGTGG
351 GTCAGTGACG TGGATGAGTA CGCACCAGAA GGCGTCCAGA AGATCCTTAT
401 TGGGAATAAG GCTGATGAGG AGCAGAAACG GCAGGTGGGA AGAGAGCAAG
451 GGCAGCAGCT GGCGAAGGAG TATGGCATGG ACTTCTATGA AACAAAGTGCC
501 TGCACCAACC TCAACATTAA AGAGTCATTC ACGCGTCTGA CAGAGCTGGT
551 GCTGCAGGCG CATAGGAAGG AGCTGGAAGG CCTCCGGATG CGTGCCAGCA
601 ATGAGTTGGC ACTGGCAGAG CTGGAGGAGG AGGAGGGCAA ACCCGAGGGC
651 CCAGCGAACT CTTGGAAGAC CTGCTGGTGC TGAGTCCTGT GTGGGGCACC
701 CCACACGACA CCCCTCTTCC CTCAGGAGGC CCGTGGGCAG ACAGGGGAGC
751 CGGGGCTTTG CCCTGCTGCT GTCTCTCGT GTGATGACCC TATTGAGTAT
801 CAGTAGCCAC TACTCCCCCT GCCTGGCCCT GAGAGCGGCT CTGCTGTCAT
851 CTCAAGCAGC CCCTGTCCCC AGCCCGTCCA CCCTGGAGTG GTCTTCTTCA
901 GCCTGTTTCC CCAGCCACAG GCCTGCTACG ACCCCACAGA TGTGCCGCAA
951 GCACTGTCTC ACCATCCGCG ACCCACCAGA CAACAGCCAG GGCTGGAGTC
1001 CAGGCCACTT TCAGCTGCTC CTTTCTCCGT GCATCGTGTC TCTTCTCTGC
1051 TTTTCTCTC TTCCCCACT TCTCTTCTC TGACCCCTCC CCTCCGGTGC
1101 GTTTCGTATC AAAGCTCCTC AAACCCCGTC CCCCCTGTGT CCTGCTGTGT
1151 GCAGCTCGCT CTTTCTTCC TTCTTAAGCT ATCCAAGGGG ATGGACCCAG
1201 GCTCGTGGGG AGGTTCACAC CTTGGATCCA GGAAGAACCC TCCACCCTGC
1251 CTCGTGGGTG GGCCAAAGGC TACAGGGTGC TTCTTCTCT TCCCCACCC
1301 CCACTGTCCC TCATGTGCCA TGGGCCTGCC TCCCCAGTGA CCTGCGAAAG
1351 TGGAGCATCG AGGTAGGAGG GAAACAGCAA CCGGGGAGTC CTCGAGCCTG
1401 GGGCTGCCCT ACCTTACCC ATTCCCGAC CAGAGCTTTG CCCTTGCTTG
1451 GCTGCCCGCC TGCCCTCTTG GGGAACTGAG CTCAGAGGCA GGTGCTTCAG
1501 AGAAGGAAAC AAAATGAGGG GTGGCAGGGA TAAAAGTCA CCTCCATTCT
1551 CTACCTCCCA TGCAGCATGA ACACAATTTC TCTCCACCTG GCTCCCAAAT
1601 TTAAAGATGT GGACCAAGGC CTGTGGGTAC TCCAGGGGCA AGGAGAGCCC
1651 TGGGGTCAGT GACACTGTCA GGCCAACCAT GCAC'TCCACA AAGGGGAGCA
1701 TTTGGAATG AAGGACTAGC TCCTATGTAT CAGGTTAAGA GCAAGGGAGA
1751 GCTGGCCAGG GACAGCAGTT TGCACAGCAG AGGGGAATGT AGCAACAGCA
1801 GGGCCTCCTA GGCCCCATCT TCCATTCTT AGGTAAGAAG AGCATTTCCT
1851 CAGACTCCCA GGCGGAGGAC TGAGCCTAGC CTTACAGCAAC CAAGGTTCTC
1901 CTGGGACCCA AAGTTTATGG GAGAAGGGCA AAGACTTCAT GGGAAAGAGG
1951 AAGGAAGGCC CTGGGTAGAA ACGCTTGGTG CTGTTCTCTT TGGCCTTTAA
2001 GACAAAGCGC TCATCTTGCC CTCTACCTCC TGATAGGCTT GAGGGTTTGC
2051 CAACCACACT GTGGCTACAG GTGGAGGGAA GAGGACTCCT TCCTCCAGAG
2101 TGCTATGTTT AGGAAGTTTC TTTAACCCCA TATGGCCCAA GAGTAGCTCG
2151 TAGGAGGCCC TTTAAAGACG GAACAAGTAA TTTACCAGTT CTAAGGGGT
2201 TCCTGCCCAC CGTCCCAAGG TGGGCGAGGC CTAGGAAGAG GGTCACTCTT
2251 AAGCCACACA TTAGCTGCAC TGCGTGGCTG CAGCCAAAAC AAAGAAGTGG
2301 GTGTTGAGTA TTCATCAACT AAGAACCAAA ATCCAGGGCA CTCATATGTG
2351 AAGGATAAGA ACCTCACTTC CTTACTCCTC CAAAAAGAAG TGGGGAAAGA
2401 ACCATCAAAC CTTTCTCCT GACTTACCAA ACCAGGAAA CAGCAGGAGA
2451 GGGTGGCTCA GGACTTAGGG ACAGGGTATA GCTTAGATGG TGGAAAGCAA
2501 AGGAGAGCAG GAAGTTGTAA ATCACTGGCT AATGAGAAAA GGAGACAGCT
2551 AACTCTAGGA TGAAGCTGTG ACTAGGCTGG AGTTGCTTCC TTGAAGATGG
2601 GACTCCTTGG GTATCAAGAC CTATGCCACA TCACACTGGG GCTAGGGAAG
2651 TAGGTGATGC CAGCCCTCAA GTCTGTCTTC AGCCAGGGAC TTGAGAAGTT
2701 ATATTGGGCA GTGGCTCCAA TCTGTGGACC AGTATTTTCA CTTTCCCTGA
2751 AGATCAGGCA GGGTGCCATT CATTGTCTTT CTCTCCTAGC CCCCTCAGGA
2801 AAGAAGGACT ATATTTGTAC TGTACCCTAG GGGTCTGGA AGGGAAAACA
2851 TGGAATCAGG ATTCTATAGA CTGATAGGCC CTATCCACAA GGGCCATGAC
2901 TGGGAAAAGG TATGGGAGCA GAAGGAGAAT TGGGATTTTA GGGTGCAGCT
2951 ACGCTCACCC TAAACTTTTG GTGGCCTGGG GCATGTCTTG AGGCCAGAC
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FIGURE 1A



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3001 TGTTAAGCAG GCTCTGCTGG CCTGTTTACT CGTCACCACC TCTGCACCTG  
3051 CTGTCTTGAG ACTCCATCCA GCCCCAGGCA CGCCACCTGC TCCTGAGCCT  
3101 CCACTATCTC CCTGTGACGG GTGAACTTCG TGTACTGTGT CTCGGGTCCA  
3151 TATATGAATT GTGAGCAGGG TTCATCTATT TTAAACACAG ATGTTTACAA  
3201 AATAAAGATT ATTTCAAACC ACCAAAAAAA AAAAAAAAAA AAAAAAAAAA  
3251 AAAAAAA (SEQ ID NO:1)

**FEATURES:**

5'UTR: 1-44  
Start Codon: 45  
Stop Codon: 681  
3'UTR: 684

**Homologous proteins:**

Top 10 BLAST Hits

|  | Score | E     |
|--|-------|-------|
| CRA 335001101587561 /WO200058473 /org=Homo sapiens /taxon=9...     | 428   | e-119 |
| CRA 18000004937398 /altid=gi 464561 /def=sp P35289 RB15_RAT RAS... | 423   | e-117 |
| CRA 18000005187045 /altid=gi 7498104 /def=pir  T33855 hypotheti... | 220   | 6e-56 |
| CRA 18000004929618 /altid=gi 131798 /def=sp P24407 RAB8_HUMAN R... | 216   | 1e-54 |
| CRA 335001098683352 /altid=gi 11422744 /def=ref XP_001482.1  TR... | 214   | 4e-54 |
| CRA 18000005096141 /altid=gi 2317272 /def=dbj BAA21744.1  (AB00... | 214   | 4e-54 |
| CRA 18000004952869 /altid=gi 131848 /def=sp P22128 RAB8_DISOM R... | 212   | 3e-53 |
| CRA 335001098688905 /altid=gi 11432830 /def=ref XP_007682.1  RA... | 211   | 4e-53 |
| CRA 18000004945380 /altid=gi 131847 /def=sp P22127 RAO1_DISOM R... | 211   | 5e-53 |
| CRA 18000005163099 /altid=gi 7705849 /def=ref NP_057215.1  ras-... | 210   | 6e-53 |

BLAST dbEST hits:

|   | Score | E     |
|---|-------|-------|
| gi 12333507 /dataset=dbest /taxon=96... | 626   | e-177 |
| gi 12120217 /dataset=dbest /taxon=96... | 377   | e-102 |

**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|12333507 brain

gi|12120217 epid\_tumor

From tissue screening panels:

Fetal whole brain

FIGURE 1B



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1 MAKQYDVLFR LLLIGDSGVG KTCLLCRFTD NEFHSSHIST IGVDKMKTI  
51 EVDGIKVRIG IWDTAGQERY QTITKQYYRR AQGIFLVYDI SSERSYQHIM  
101 KVVSDVDEYA PEGVQKILIG NKADEEQKRQ VGREQQQLA KEYGMDFYET  
151 SACTNLNIKE SFTRLTELVL QAHRKELEGL RMRASNELAL AELEEEEGKP  
201 EGPANSSKTC WC (SEQ ID NO:2)

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

205-208 NSSK (SEQ ID NO:6)

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 2

1 92-94 SER  
2 206-208 SSK

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 2

1 29-32 TDNE (SEQ ID NO:7)  
2 104-107 SDVD (SEQ ID NO:8)

[4] PDOC00007 PS00007 TYR\_PHOSPHO\_SITE  
Tyrosine kinase phosphorylation site

101-109 KVVSDVDEY (SEQ ID NO:9)

[5] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 2

1 18-23 GVGKTC (SEQ ID NO:10)  
2 136-141 GQQLAK (SEQ ID NO:11)

[6] PDOC00017 PS00017 ATP\_GTP\_A  
ATP/GTP-binding site motif A (P-loop)

15-22 GDSGVGKT (SEQ ID NO:12)

[7] PDOC00579 PS00675 SIGMA54\_INTERACT\_1  
Sigma-54 interaction domain ATP-binding region A signature

11-24 LLLIGDSGVGKTCL (SEQ ID NO:13)

FIGURE 2A



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**BLAST Alignment to Top Hit:**

>CRA|18000004937398 /altid=gi|464561 /def=sp|P35289|RB15\_RAT  
RAS-RELATED PROTEIN RAB-15 /dataset=nraa /length=212  
Length = 212

Score = 423 bits (1077), Expect = e-117  
Identities = 207/212 (97%), Positives = 209/212 (97%)  
Frame = +3

Query: 45 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 224  
MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ  
Sbjct: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG 404  
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG  
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG 120

Query: 405 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 584  
NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL  
Sbjct: 121 NKADEEQKRQVGREQGQQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHRKELEGL 180

Query: 585 RMRASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)  
R ASNELALAELEE+EGK EGPANSSKTCWC  
Sbjct: 181 RTCASNELALAELEEDEGKTEGPANSSKTCWC 212 (SEQ ID NO:4)

>CRA|335001101587561 /dataset=GENESEQ /org=Homo sapiens /taxon=9606  
/mol\_type=protein /date=08-FEB-01 /length=218  
/altid=derwent\_id|B41604 /altid=derwent\_ac|B41604  
/def=Human ORFX ORF1368 polypeptide sequence SEQ ID  
NO:2736 /patent=W0200058473-A2 /pat\_section=Claim  
Length = 218

Score = 428 bits (1088), Expect = e-119  
Identities = 212/218 (97%), Positives = 212/218 (97%), Gaps = 6/218 (2%)  
Frame = +3

Query: 45 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 224  
MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ  
Sbjct: 1 MAKQYDVLFRLLLLIGDSGVGKTCLLCRFTDNEFHSSHISTIGVDFKMTIEVDGIKVRIQ 60

Query: 225 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG 404  
IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG  
Sbjct: 61 IWDTAGQERYQTITKQYYRRAQGIFLVYDISSERSYQHIMKWVSDVDEYAPGVQKILIG 120

Query: 405 NKADEEQKRQVGREQGQ-----QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 566  
NKADEEQKRQVGREQGQ QLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR  
Sbjct: 121 NKADEEQKRQVGREQGQKCPQLAKEYGMDFYETSACTNLNIKESFTRLTELVLQHR 180

Query: 567 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 680 (SEQ ID NO:2)  
KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC  
Sbjct: 181 KELEGLRMRASNELALAELEEEEGKPEGPANSSKTCWC 218 (SEQ ID NO:5)

FIGURE 2B



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Hammer search results (Pfam):

| Model   | Description                    | Score | E-value | N |
|---------|--------------------------------|-------|---------|---|
| PF00071 | Ras family                     | 323.8 | 8.2e-95 | 1 |
| CE00060 | CE00060 rab_ras_like           | 211.0 | 1.8e-59 | 1 |
| PF00006 | ATP synthase alpha/beta family | 4.2   | 2.1     | 1 |

Parsed for domains:

| Model   | Domain | seq-f | seq-t  | hmm-f | hmm-t  | score | E-value |
|---------|--------|-------|--------|-------|--------|-------|---------|
| PF00006 | 1/1    | 10    | 24 ..  | 203   | 217 .. | 4.2   | 2.1     |
| CE00060 | 1/1    | 2     | 165 .. | 16    | 184 .. | 211.0 | 1.8e-59 |
| PF00071 | 1/1    | 10    | 212 .] | 1     | 198 [] | 323.8 | 8.2e-95 |

FIGURE 2C



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1 GCTCAAGATT GCACAGCTGG TGAGTGGTGA CACTGGGACT GGAACCCAAG
51 TGTGCCTTAC TCCAGAGCCC TTGGCATGCA CCTGAAACCC CATGTAAGCC
101 CACTGTGGAG ACGCGCACCT CGAAATAATG GAATCCACTA CATCAGTTCC
151 TTTAGCTTTC TGTGTAATCA GAGTAGCTAG CAGGCTCGGG ATTTGCCCCC
201 CCGGCTTTTT TTTTTTTTTT TTTTGTAGAC AGAGTTTTCG TCTTGTGGCC
251 CAGGCTGGAG TGCAATGGCG CAATCTCGGC TCACCGCAAC CTTGCGCTCT
301 CAGGTTCAAG CAATTCTCCT GCCTCAGCCT CCCGAGTAGC TGGGATTACA
351 GGCACCGGCC ACCACGCCCA GCTAATTTTT TTATATTTTT AGTAGAGATG
401 GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTTTTCC CCTCTTATTA
451 TAATTCAGAC ACTTAACCTG AAATATACCT TTTCAAATGA AGTAAATGGG
501 CTTACCACTT TCCTTGACCT ACTATTGAAA AATACATTCT CCATCCAATA
551 TTCAGCCTGA AACACGGTAT GTACATATAT ACTTTTCATT GCTTTTTTTT
601 TTTTTTTTTT GAGACAAGGT CTCCCTCTGT TGCGCAGGCT GGAGTGCAGT
651 GTCATGATCT CGGCTCACTG CAGCCTTCCC CTAATGGGTT CAAGCAATCC
701 TCCACCTCA GCCTCTCAAG CCTGGGATTA CAGGCGAGCC ACCGTGCCCA
751 GCTAATTTTT TTTTATTTTT AGTAGAGACT GGGTTTCACT ACATTGGCCA
801 GGCTGGTCTC CAGCTCCTGA CCTCAAAGTG ATCTGCCCCG CTCAGCCTCC
851 CAAAGTACTG GGATTACAGG CATGAGCCAA CGCGCCTAGC CTTTCATGTC
901 TTTTTTAAAG CCTAATAGGC TAGACTTTCG TCTCCCTCAA TACTCGTTGG
951 TAGGGATAGG CAATTTTCTC AACTCCGGAG AGCATTTCATT TGCCTCTCTC
1001 CGGTGCTAAC ACATTCAGTG GTAGGAAACT GGATCTTGAA CAAGGGCCAT
1051 TCATTCCTTG GTGCCACTGG CTATACCACA GAGAAATTTA GGGGTCTGAA
1101 ACAATACATT GGTCACCTGG GCACCTATCC TAAGCACCTT AGAGGGAAAA
1151 CGGAGACTTG CCCGCACACC TCTAAAGGAT TTTGCACTTG GAGATGTTCT
1201 TATGGCCATC TATCTTTTCA CCCTGGTGGA GGCCGTGAAT AGGCATTTTC
1251 CCCATTTAAA GAAAAAATGG GGACGGGGGA GGGCCGTGAC ACAGTCACAC
1301 AGGTAAGGGG CAGCCAGATG GCAGGGAGGG GGAATTCCAC CCACACTCTC
1351 GGGGACTCAT GGAGACGGGT GTTCGAATCC AGATCCTGCT CAAGGCCTTC
1401 CTACCTCGGG TGAGCCAGC TGAGGTACCA GCCACTGGGG AGCCCCGCCA
1451 GATCCTGCAG ATGCAGGGTG CCACGGCGGG CGGAATTACC GGCGCCAGAC
1501 TTGGGGTGGG ATATGGGGAG AAGTGGTGAG CCCGAAAAGC GGAGCACGGT
1551 AGAAGTGGGC TTGGTGGGGG CTCACCTCAA CTCCCCATT CGGAGCGTCC
1601 GCGGAAAAAC GAAACGTTT CCCC GCCCGG GGCAGGAAGG GGTTGGGAGG
1651 GGGGGCTGGC GCCCCGCCCC AGCGTCGCCT GCTCGATGGG GTCCCGCTCT
1701 CCTGCGCGCG CTCCCCGCC CCTCTTACC GGGGCGGCGG CGGCGGCGCA
1751 GGGGAAGGGG CGGGCAGGGG CCGCCGCCGG TTTCTCTCC CACCGCCTCG
1801 CGCCAGCCCA GCCGAGCCGA GCCGAGCCGA GCGGGCGCCG CGCCGGGCTC
1851 CCGCCGAGC CGCCTTCCC GGCACCCAGC GAGCGAGTGG GCAGGCGGGC
1901 GGGCGAGGCA CCGCGGGGG CCGGGCCCGG CGTCCTCTC GCCGCCGCA
1951 GCGTCCCCGG GCGGGCGCGG GCGCGATGG CAGCGGCGGA GCAGGGCTGA
2001 GCGCGTGCC CGCCCGCAGT TCCCGGCCCC GCTGGCCCCA GTCATGGCGA
2051 AGCAGTACGA TGTGCTGTTC CGGCTGTGC TGATCGGGGA CTCCGGGGTG
2101 GGCAAGACCT GCCTGTGTG CCGCTTACC GACAACGAGT TCCACTCTCT
2151 GCACATCTCC ACCATCGGTA AGGGGCGGTG GCGGGGGCG CCCCTCCCTC
2201 CCGCCCGCGC GCGCTTTCC CCGCCGCCCC CGTCCCGAGC TGGGGAGGAA
2251 TTGCCAGCCC CTCCGGCTGG AGGCGGTGGC GCGGAGGCC GGAGTCCGGG
2301 ATAAATCTCG GGGTGAGCAT AGGTTTTGGC AGGTGAGGGT GTCCCTGCTG
2351 CCTGCCGTCC GGACCAGGGG TGGGGTCTCC CGCCTCTTGC CGGGAAGCCT
2401 TCCGTCCCAT CAAACCGAGA AACCAGGGGT GAGGGGAGCT GGTGTAGGCC
2451 TGGGTACCCC GAGCTGGGGT AGCAAGAATC GTAGCCGCTG GAATAACACC
2501 CCCACACCCC CAGGGGGAGG GGAAGTAAAG CTTCTGTCTAC GGAAAAGGGG
2551 GTCAGGGTGG AGACCGGAGT CACTGAGGCG CCCTTGTTTC TGTGGTGACC
2601 CAAGGTGGAG CCGGCGGGGG GCGAGGGGGG GAAGAGAGGA CGTACGGAGG
2651 GGCCACAGGG ATCGAGTTTC CAGGGCAGAG TTGGGAAGGT AAGCCGCAAG
2701 GTGGGACACC TGGGGGAGGA CACAGATAGG GTGAGGAGCC CCTGCGCTG
2751 GGAAGAGGAG ACATCTGTTC TGAGGGAGGC TAAAGAGGAT GGAGGAGTGT
2801 CAGGAATACC TGCCCAGACC AAGGGTCTAG AAGGCAGGCA GGACCCGCTT
2851 GAGGCATCT CTCATCTGGC AGTGCTGGAG CCTGTGGTTA GAGGGACAAG
2901 ACCCGGTGGC ATCCAGACA GCACTATGAT GGGGTCACTT ATTCTAGGAA
2951 TGGGTCCATG GCCTCCCCCTC TGAGACAGTC AGTCTCCCGC TTCTAGGCTG
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FIGURE 3A



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3001 TGAGGGGCCC CCTCCCTGAG AAGTCTGAGT AGAGGGAATT TCATCCTCAG
3051 CTGCTACCCG GGTCAGCCCT GGAGTAGCCT CTGCATTGCC CAAGCCCTG
3101 GAAACACCTG CTGGCTGGCT GGTCATCCAT TTGGAATGCT CTCCTAGAAG
3151 TCCCTGCTGC CATCAGGGAT GGGCACCAGC TCTCAGCTTC CTCTTGAGGA
3201 TTCATGTCCA CACCATCCCC CCTCCCCCA ACACACATTC CTTGCTGAGA
3251 GAGAAGTAGG AGCAGATAGA TACAGCCAGG AGGAACAGAA CCTTCTGGTT
3301 AAGAAGCCAG CTTTATTGTC CAAGAGACCT GAGACCTCAC TGTGGGGCAA
3351 AGCAACCTTG AATATTGCCT AAACCTTCTGA GCTTTATTTA GTTTCTCATC
3401 TGTAGAACGG GTATAATAAT TGCACCTACC TGCCAAGTTG TTGTCAAGAT
3451 TAAATGAGAT AACGATTGTT AAGTGCTTAG CACAGCCAGA CACATGGTGA
3501 AGCTCGATAA ATGCTGATTG TTCTTACTGC TATTGCCATT ATCATTGAGC
3551 TTTTAGGGTC TCCTCTCTTT GTTTCACCAA CTTGAAGGGT GAAACAACAG
3601 GACTTAGGGT CAGGGAACAG AACTTGTCCTG TCTTTCTCAG AGGAGCTGTA
3651 AGGCCAACTC TTAGGAAACC CAGGAGCTTG GGCTGAGCCA TGGTTTGGAT
3701 GAGAGACATT GCAGAAAGAA GGGGAGCCTA TAGACACTAA GGCTTTGTGC
3751 CTGCCGGGAG GACTTGGGGA AGAGGCAGGT GCAGGAGAAA GGCAATGGCG
3801 TGATGGAGGA AGTGGCAGAG GAACCAGATG GTGTATGAGG ACAGGTTGTG
3851 GGCTCAGGGA CAAAGGGCGG TGGGTTATCC CTTAAGGAAA CTAGGAGTGG
3901 CTATTTTGGG GAGAGGCCTG GTGCTTGGA CTACTGAGCT ATCTCCAGAG
3951 AGCTGTGGGC TGCCTGGGAG GCCCTGGCTT TGGCCTGAAG AGCTGTTGTT
4001 TGCACCTGCT CTCCTAGTCC CATTCCAAGT CCTATAGGTG ACATGGACTT
4051 TTCCCTTTGA GGGCTTCATT CAACCACCTC ATTTCAGAAG CTCTGGGACT
4101 CCTGCTTAGT GCTGTGGGAG GCAGCCTCCC CTGGGAGACA CATACCCTCC
4151 TTTTGTAGGG CACCCCTCTT TCTAAAATAC CAGGATGGCC CTCTGAGGCT
4201 CGTGCTCTCC TTAAGAGAG TCCATTGCCT CACACCTCTA ATCATCCACC
4251 CTTCTCCTTG TCCCTTCCCC TTGTAATCTC CTTTCTTAGA CACCTTCTGC
4301 TAATAGGTGA ACATAAATA GGTCACAGGG ACTTCCTGAA ACCCTCCAGG
4351 GCAGACCACT TTGGGCACAT AGGTGAATCA GTGAACTGAG TAGGGGTGTC
4401 TCTGCAGCAC TGTCTCCCTT CAAGGCCCTT GGTATATTGG CCTAAACCTT
4451 AAAGATGGCT CCCAGATTTC TTCCTCCGCT TCTGACACCC GGGTTCCTCT
4501 TTCTACAGGA CACAGAGGAT TCTCTAGGGT CCCCCTTTC ACAGGACACA
4551 GAGGACTCTA GGAGTTTGGG TTCCATGGAA TAGAAAAGAAA CCTGTCTTTC
4601 TTCACACCAG CTTTTTAAAA TCTGCCCCAC TGGGTATCTT AAATGCTTTC
4651 TTATTTAAAG CTTATTAAAG GACTTGGGAT TCTCCCTTAT CTTGGGCGTG
4701 TTTTTCAGCA TTAATAAAA CTTAAAGGAA AGAGTTGGAT GGTCAGAGAA
4751 AGCTTTTTC TTAAGTGATA TGGACAGTTT CTCAAGGAGG TAGAAGGGGC
4801 AGCCAGGAGA CAAATCAAGG AGCCAACGAA ATGAGTGCTA CCAAGTCATA
4851 GTCATTGCTT TATTTTAAA AAATGCGTGT CCTGTATGCC AGGCTCTGCA
4901 CTGAGACCGA GAGATTCCAA GATGAATAAT ACCTACAGTC ACTGTTCTCA
4951 AATTGTGCAT TACCTAAAAC ACATTACATG ACCATGCTGG CCACTGATCG
5001 AGGCACCTTT CCCAGGGGCT TTTTTTGTGA ATTAAGAAAA CAAGGTAATT
5051 CACCAGTTAT TGCCAAGATA GTTTGGCTTC TTGGCTCATG TGGATATCAC
5101 CTAGGCCAGT ACTTTTGTGA TTTACTGTGT ACTCCACTTT AACGGCCTGC
5151 GATCTTCTAG AGAAGAACCC GCCAGGGAGC AGTGAGAGGC CTCCCTGGTA
5201 GACTGAGACA CTGACTGTCC CTCCCCTAT CTTTTCTGTC TTTCTGGCCA
5251 GCAGACCAGC AGGTGGCCTT GCCACTGCTC CTGCCACAGG CATTTCCTTT
5301 CTGTGCAGCT GTGCTGGCCT GGCTGGGGGT TGGTGCGAAG GGGTCCCCAA
5351 AATACTACCT TAAACAAATT AATTGAGCAT TCACTACCAA GCTCTGTGCC
5401 AGGCATTTTA GAGACATATT GCAGTCTACG TTTTCTGCCC ACAGAAGCCC
5451 ATAACCTAGA TGGGGAGGCA AGACAAAGGG AAAACAAAA AACAAAGAGC
5501 TAGTGCCAAA ATGAGATATC TGAAAGAACT TGGTGAATCA CTCTCAAAT
5551 GTAAAGGATG GATTATGATC ATTGCAGTTA CTCTTAATGA AGGTCTCACA
5601 GTGGGTATCA GAAGCTAAAT TATGATGCAA GATGTACCAT GAGGCAGCCG
5651 GAGAATGGCG ATGGATGGGA TGGGTGAGTG CTATTCCCAC GACTCCATGC
5701 TGTGCGAGGC TGGGGAAGAG AGAGGCCCTT GTGGACTAGA ACCGGCAGGG
5751 AAGGCTGAAG CTAGGCCCTA GTGTGGGCTG CTCGTAGTT CCTGCAGCAG
5801 AAGGGAGCAG ATGGAGTAAC ATGAGCAGAG ATAACAGAGG TGGGATTGAG
5851 TAGGTGTCCG TGGGCTCTA GGCAGTTTGA ATGCAACAGA AGGGATTCTT
5901 CAGGAAAGTG AGAAGATTCT TCTGTTTCTC TCTCTGTCTC CCAAATTATA
5951 AGTGCCTTGA TGGTGCAGCC AAATCTTATT CCTCATTGTT TTTATAGTCC
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FIGURE 3B



Docket No.: CL001188  
Serial No.: 09/817,198  
Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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6001 CTAGTACAGG GCCAGGCAGA TTCAATGCCT GTTGTTAAAT TAATGAATGA
6051 ATGCAGGGAC CAGTTGGCAG AGGGCATTGA GAGCCTGGCC AAGGAGGTGG
6101 AACATGAGCC TTAGCAATGG TAGGAGGGGT TTTGAGTAGG GTACTAATGA
6151 GGTTGGCTGG AAGAAGGGGT TAAGACTTGA AGCAGGGAGA CTAGTCAGGG
6201 GCTGCAGTAG TATCCTGGGC ATGAAGGAAC CTCTGAATGG CCCCTCACCC
6251 CCAGTGGTAC CAACACCAAC TTCCACACAG TCAGTTGTTC TACTTTCCCT
6301 CCAGAATGGG GAGTGGTTCA AGCCAATCAA CCTGGCAACT TCTGAAAGAA
6351 TCTTATGGGA CCTGTGCCAT GACCAGGTAG GGAGAAGATG TCATACATGG
6401 ACATCTATGT TCAGGGGACC TTTGAGGACC TTTCTGCATG GTGGCCAGGA
6451 GTGAGATGAT GTAAACCACA AATGGAAACT GAAGAGACTG CTCAGGAGTT
6501 GTTGGTTTTT TTTTCTTTTC TATTTTTTTT TTTTGTAGAC TAGGTTTCAC
6551 TCTGTACCC AGTCTGGAGT GTGGTGGTGG CACAATCAG GCTCACTGCA
6601 GCCTCGATCT CCTAAACGCA ATCCTCCAC CTCAGCCTCT CAAGTAGCTG
6651 GGACTACAGG TGCATGCCAC CACATTCAGC TAATGTTTGT ACGTTTTGTA
6701 GAGATGGGGT TTTACTATGT TGACCAGGCT GGTCTCGAAC TCCTGGACTC
6751 GTGATCCACC AGCCTCAGCC TTCCAAAATG CTGGGATTAT AGGCGTGAGC
6801 TACCTCACTC CCTCAGGAGT TGGTTTTCTC CCTCCCATCC TTAGTCTTCC
6851 CTGAGTAGAC CTGTACACCA GTCCCTGGAC CTTTTGTTTT GAAAGCCACC
6901 CTCCAGGCTA CACTCCTTCT GGGTGAGGAG GAGGGTGATC TGGTTGGACA
6951 GGTTGGGGCTG CTGTGGCTTC AGGGCACTTT CTCAGGCTGG GTTGCTGCTG
7001 CTATGTCACC TTTCTCAAGG AGTTCCTGCTG GGACTGGCTT GGCTGCCTGT
7051 CTTGACTTTG CTTTTGACTG AGGAGGTGGG AGATGGTGAG GGAGGGGGTG
7101 GGGCTAGATC CAAGCCTGGA ATGGGGTGAC CTAACAGACA CTGGGGCCTG
7151 TGCTTAGACA CTAGGATCCT GGGGTTTTGCA GGTTTCTAGA CTGAGAGGAG
7201 CTGGGGGCAA ATGCAGTGTG ACGTTGTGAG AGGGTCAGGG CTGGGTCTGT
7251 GTCAGCCTTC AGGCAGCCTG AGACCAGTCT CTACCTACTC TGTTCCTCTG
7301 GTACCTAGAA AGGAAGGGAA GGTGAGAAGC AATGAGCAGA ATGGAAAGAG
7351 CCCAGATTAA CATGCACATT TCCCATGGCC TTAGTGCCCC TGTGACCTTC
7401 AGACACTTTG ATGACATCTT TGTGCTTCGT TTCTGCATCT GTAAATTGAA
7451 GATGGTAACA GAGTCTTTCT TAAAGGTTGT TGTGAAGATT ATAGAGCCTA
7501 GCGCATATAA AGCACTTGGC AGAGCCCTCG ATAAAATAAT AGCTGCTATC
7551 ATATTATCAT TATTATTATT TTATTTATTT ATTTATTTAT TTTTTTTTGA
7601 GACCGAGTAT CTCTCTGTCTG CCCAGGCTGG AGTGCACTGG CACAATCTCG
7651 GCTCACTGCA ACCTCCATCT CCCGGGTTTA AGTGATTCTC CTGCCTCAGC
7701 CTCCTAAGTA GCTGGGATTA CAGGCACCCA CCACCACACC CGGCTATTAT
7751 TATTATTCCT AGCTATAAGA ATGCTGTAGA GATGAATACA CTGTCAGTGA
7801 GCTAGGAGGT CATCCTGTGT ATCCATCACT TGTGCACTCA GTCGTTCAAG
7851 CGCTATTTGC TGAACACCAA CTACATGCCA GGTGCCATGC TAAGATTGAG
7901 GGACACAGTG GTGACCAAAA CAGACAGAAA CCAAGGAGCT GGCTTACATT
7951 CCAAGGGAGT GCATAGGAAG CTGTGTTTCA TTTCAGTTTC TGCTCTAGTA
8001 CCCCCCTTTC CCTGGCAGTG CCAGGGTCTG AGAAGGAAGA GTGAGGTGGT
8051 GAGGAGGTGT GAAGCAGTGG GGTGACCTGA GAGGAGAGGA TGGGGTGGCT
8101 TTGCCTCAAG GCTTGGGCCC CTGCTAGGTG TCGCTCTGCC TCAGGCCTCT
8151 GTTTCTCCTC CTGACACAGG CACAGACTCG GCCTCCCACC CCTTCCCCAA
8201 GGACATGACC TTGGGAAGGA ACATATCTGA AGCCCGCGGA GGGTTTCCGC
8251 TGCTGTGCAT CTGTGCCACA GATCCGCAGA TGCACCACA GCTGGGAGCA
8301 CCGGTTCCCTC CCGCCTACCT GCACTCCCTG GTTTCTGTTC CTTCTCCTC
8351 CTCCTTCTCT CTCCCCGCTC CCCAGACAGG CTGGTGATGA GCTTTATAAC
8401 ATGAAAGCTG ATATTTGGCC ATTATCCTTC TACCCTGATT GCCAGCTCTT
8451 CTCAGAGTGC CTTCTTCTGT AATCCAATCT TTGCACCACT TTCCCTGTGA
8501 AACTGCCAGT TTTCTGTATA GGCCTCTGCC CTCTCCTTGG CTCTTCTCTC
8551 TGGTCACTGA GCTTTGTCAA GGGGAACACA GGGCTTCTCT GACACGTAAT
8601 TCCTCCCACT GAGGAGGAAG GGGCTAATCA CCAGCCCTGT TTTATTTTAT
8651 TTTATTTTTT TGAGATGAAG TCTAGCTCTG TCGCCAGGC TGGAGTGCAA
8701 ATGGCTCGAT CTCGGCTCAC TGCAACTTCT GTCTCCCGGG TTCAAGCGAT
8751 TCTTCTGCCT CAGCCTCCTG AGTAGCTGGG GATTACAAGC ATGCACCACC
8801 ACACCTGGCT AATTTTTTGT GTTTTTAGTA GAGATGGGGT TTCACCATGT
8851 TGGCCAGGCT GGTCTCGAAC TTCTGACCTC AGCTGATCCA CCCACCTCGG
8901 CCTCCCAAAG TGCTGGGATT ACAGGAGTGA GCCACCATGG CTGGCCGACC
8951 CCATCTCTTA AAAAAACAAA AAGAAAAGAA AAGAAAACAA AACAAAAACA
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FIGURE 3C





Docket No.: CL001188  
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Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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9001 CTTTTTAAAT TAACTGATTA TGGTGGCATG TGCCTGTAGT CCTAACTACT
9051 CAGGAGGCTG AAGTGGAAGG ATTGCTTGAG CCCAAGTAGT TGGAGGCCAC
9101 AGTGAGCTGT GATCACACCA CTGTACTCCA GCCTGGGTGA CAGAGTGAGA
9151 CCCTGTCTCA GGAAAAAAAA AAAATTACTG AGAACTCTGT GACCATGGCA
9201 CCATGAAC TAAGAAAGGCG TAACAGTTGG CTTTGAAATG TGGGTTATGG
9251 CTGGGTGCCG TGGCTCACGC CTGTAATCCC AGCACTTTGG GAGGCCAAGG
9301 TGGGCAGATC ACAAGGTCAG GAGTTTGAGA CCAGCCCGGC CAACATAGTG
9351 AAACCTCATC TCTACTAAAA ATACAAAAAA TTAGCCGGGT GTTGTGGCAG
9401 GTGCCTGTAA TCCTAGCTAC TCGGGAGGCT GAGGCAGGAG AATTGCTTGA
9451 ACCCAGGAGG TGGAGGTTGC CACAAGCTGA GATCGCACCA CTGCACTCCA
9501 GCCTGGGCGA CAGAGCAAGA CTCCATCTCA AAAACAAAAA TAAAAACAAA
9551 AAAAAGTGGT TTCTTTTCTT TTCTTTTCTT TTTCTTTTCT TTTTCTTTCT
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9651 CTCAGCACAC TGCCACCTCT GCCTCCCAGG TTCAAGTGAT TTCCCTGCCT
9701 CAGCCTCCAG AGTAGCTGGG ACTACAGGCA CGCACCACCA CGCTGGGCTA
9751 AGTTTTTGTG TTTTAGTACA GAAGGGGTTT CACCATGTTG GCCAGGATGG
9801 TCTCCATCTC CCTGACCTCG TGATCCGCCC ACCTCGGCCT CCCAAAGTGC
9851 TGGGATTACG GGCATGAGCC ACCACGCCCC GCCTAAAAGT GGGTTATTTT
9901 CTAATTGCTC TTCCCTGATT AAAATTTTCT CTTTGCCCAT CTTTCTCTTA
9951 GATATGTACT GACTTCATTC ATCCATTAT TCGTCTCACT TGCTCATTTA
10001 TTTTGTCTTT CATTTACTCT ACTTTGTTGA ATAATATTTA GTGATCTACC
10051 TGCTGCCAGG CAGTGAGAGT CTGAAGTGAA CAGGATGCTG CTTTGCCCTC
10101 TGGGAGCTTA CAGTGTAGCT GGGAAACCAGA CATCCAAACA AGCAGAATAT
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10201 CCCTCCCGGG GAGGCTGGTG AAGGCTTTGA AGAGGAAGTG ACATTTGAGT
10251 GGAGTCTTGA AGACTAGGCA GGATTCTCCA GGGGCCCTGG GTGTGGGGGA
10301 AGCACACATC CTCTTCCCTG TAGGAGGTGC TGTGGAGAAC ACCTCCAGTG
10351 GGGCTGCTAC TCTTCAGCCT TGCTGGGGCC AGCTGGAGTG GCCACACCAT
10401 GGTCACACCA GCTGAAGTTC AAGAAGCCCC TTGCCAGGAG ATTGCTTTGC
10451 TGGCTCTGGG TGAGGGCAGG TGCATCTGGA AGCCCCCTTC TTTCTAAGAT
10501 GTTTGCTCCT GAGTTTCTAT GTCCTAGTCT TTTCTTCCCT GAACCTTTTG
10551 CTACAGTCA GCACAGCCCT GCCTGAGAAG GAGGCTGGAG GAGTGAGTGG
10601 TCAGTAGCCT GGTGGGTCTT GGCTGCCTCT GTGGTGCCCG CTGGCCTAAG
10651 TAGCAGGCTT AGGGAGGCGA GACCCAGTTC CAGGGGCTGC CAATGGGGAG
10701 CGAGATGGGG TGGCTGGAGC ACACTGCACA TGTCACCAAG GCTCTAGGGA
10751 GGTCTGTGCA CAAGGCAGTG GGAAAAGCAA GGGGAAGACC CAGCCTGGTC
10801 AACATGGTGA AACCCGTCCT CTACTAAAAA TACAAAAATT AGCTGGGTGT
10851 GGATAGAGCA GCCTGTAGTC CCAGCTAACT TGGGAGCCTG AGGCAGGAGA
10901 ATCACTTTAA CACAGGAGGT GGAGGTTGCA GTGAGCCGAG ATCGTACCAC
10951 TGTA CTCCAG CCTGGGTGAC AGAGTGAGAC CCTGTCTCAA AAAAAAAAAA
11001 AAAAAAAAAA AAAAAGTGGG GAAGGGGAAC ACTGATCCTG ATTATCTACT
11051 CCATATACTT ACTATGTACC TACTACCTAC ACAGGGACGG TGGGCTTTAC
11101 GCATGCCATT TATTCACTGT ATAGAGATCT CAGCATCACA TAGGAGCAGG
11151 GAGTCTGTAA GTTGGCCTTG CTGGCATTTG AGAAGTTTCT TGGTGTATTCT
11201 TTCAGGTTCA CGCTCCAGA CAAGTGTAAG TGCTATTGAA TGCTGACTAT
11251 GTTCCAGGAA CTAAACCAGA TGCTAGAAGA CACGCAGTAA ACAGTACAGA
11301 TGCAGGTGCA CATGTGAGGG TCCACACAAG ACCTGAGAGA AGGGAGGGGT
11351 CTTGCTGCAG TTCCCCCTTT GTAACAAAGG AGAGAGTACT GTTGACCCCTC
11401 TTCCTAGGAA CTGTGAGTTT GACTGAAATG TGTCTGCCA CAGGATCTTT
11451 GCTGCTTCCT CTACCTGATT CTTTGGATCT CCCTGCTGGC ACCTTCTTGT
11501 CATTTAGGTC TCAGCTCAAA TGTTACCTCC TTTAAAATGT CTTCTCTGGC
11551 CAGCCAGTCT AAGTTTGCTT GTGCTTGGGG TCTCCTCACT CTCTACTTTA
11601 TCCCGCAGTT GCTTCTTATC ACATATGGCT CTCTGAAATT AGGTATTTCAT
11651 TACTTACATC TGTCTTCCCC ACTAGAATTA AGCTCTGATG ACAAGGATCT
11701 TTCTGTGCTG TTCATAGCTT ATCTTCTAGT ACCTGGCTTA GTTCCTGGCA
11751 CATTGTAAGC ATTCAATAAC AGTTTGAATG AATGAATTAA CAAATGAAGG
11801 AATGAATGAA TGCATTTTCC TAGAGGACTT CTGTTCTTCC CTGAGGGAAG
11851 TTATAGGTCG TATTGGTTTC TTGGGACTGT TTTTGTGTTG TTTGTTTGTG
11901 TTTGTTTTTT GAGACAGAGT CTCACTGTAT CCCCCAGGCT GGAGTGAGT
11951 GGCACAATCT TGGCTCACTG CAACTTCCGC CTCCCAGGTT CAAGCGATTCT
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FIGURE 3D



Docket No.: CL001188  
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Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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|       |            |             |            |            |            |
|-------|------------|-------------|------------|------------|------------|
| 12001 | TCATGCCTCA | GCCTCCCAG   | TAGCTGGGA  | TTCCAGGAGC | CTGCCACCAC |
| 12051 | GACCAGCTAA | TTTTTGTATT  | TTTAGTAGAG | ACAAGGTTTC | ACCATGTTGG |
| 12101 | CCAGGTGGT  | CTTGAAGTCC  | TGACCTCAGG | TGACCTGCCT | GCCTCTGCCT |
| 12151 | CCCAAAGTGC | TGGGATTACA  | GGCATGAGCC | ACCACGCCC  | GCCTGTTTTT |
| 12201 | TTTTTTTTTT | TAAGACAGAG  | TCTTGCACTG | TCTCCAGAC  | TGGAGTGCAG |
| 12251 | TGGTGTGATC | TCAGCTCATT  | GCAGCCTCAA | CCTCCTGGCC | TCAGGTCCAG |
| 12301 | GTGATCCTCT | TACCTCAGTC  | TTCTGAGTAA | CTGGGCCCAC | TGGTATATAC |
| 12351 | CACCACACCT | GGCTAATTTT  | TAAATTTTTT | GCAGAGACAT | GGTCTCACTA |
| 12401 | TGTTGCCCTG | ACTGATCTTG  | AACTCCTTGG | GTTCAAGTGA | TCCTCACACC |
| 12451 | TTGGCTTCCC | AAAGTGCTGG  | GTTTACAGGT | GTGAGCCACC | ATGCCTGGGC |
| 12501 | TTGAGACTGT | TAAGATGATG  | AGGCTGGAGG | GAGTGGATGG | CCTCACTGCT |
| 12551 | TGAGCCCTAG | TAAGTCTTAA  | CTCCAGAGTG | CCCTGGCTGC | AGAGGTGGCC |
| 12601 | CTGGAGGGTC | ACTCCAGCAA  | CCTGGCTGAG | CTGATGGGCA | TCATCTGATA |
| 12651 | CCAGCTCTGA | CCCTGAATAA  | TAGGCAACAT | GGACCTTAGT | CTAAAGCACT |
| 12701 | GACCCCTCAT | CTCTGCATAT  | ACCAAAGAAG | ATGAGATTTG | GGTGAGGACA |
| 12751 | CAGCCAAACC | ATATCAGCTC  | CCGGGATCCC | TGTGTGAATG | GGGTCTTTTT |
| 12801 | TGGTGTTTGA | GGGCTGCACA  | GGGTGACCTC | TTTAGAGGTG | ACCTCCTGCC |
| 12851 | ACAACCCACA | GGAGGTGCAC  | ATGGCCCACA | CATGCTGGTT | TCCTGCAGTG |
| 12901 | GGAGGCGGTG | GGGCACTCCT  | GGGACCTGTG | CTTGTTAACT | GGAGCTGGCC |
| 12951 | TGGCCCTGGG | GATTGGGTGT  | CTGCCTTGGG | TTTCAGGTGT | ATTAGGTGT  |
| 13001 | TCCTCGTTGT | GGAGTCTCAT  | TACTAATGAA | AAGTTCAGGT | CGCACTGCTG |
| 13051 | GTCTTTTGGG | CTGTGGTTGA  | TCCTGGTGAT | AACATTGGC  | ACCCAGAGGC |
| 13101 | AGCCCTGTTT | CCACTGAAGC  | ATGCGGAGCT | TGGCTGGCAG | GCAGGCAAGC |
| 13151 | TGGCAGCTGC | CCTTAACCCA  | TGAGGTGCTG | GCCCGCTAGT | AGGCACACCC |
| 13201 | TACCTGTGCC | AGAATTGAGG  | TTGTAGCCAG | ACTCCAGGAG | CCATCTGGGC |
| 13251 | CCCACAGGGG | GCGGCATTTT  | CTCTTTTGT  | TGAAACATTC | CAGCCAAAGT |
| 13301 | CTGGCTTGGG | CTTCATCTCT  | CTGTCCCACT | CTCCTTCCTC | TCCCCAACAT |
| 13351 | AAGCCTCCTT | CTACATCCTA  | GAGCTCTTTC | CATTCCCCCT | CCTGCAGCTC |
| 13401 | TGGGCTCGCT | AATCTCATGC  | TTCCCTAAGG | GAGCTTGACG | GCTGCTTCTG |
| 13451 | CTAACATTTA | ATAAAGTTCT  | GCGTGCCAGA | CCCTGTGTTA | TGGGTTTTAC |
| 13501 | ACCTTATCTC | ACAATCTTAA  | AAAAAAATT  | CTCTGAGAAT | CCTCTGTCAC |
| 13551 | CCCCACTTTA | CAGGTGAGGA  | AACTGAGGCA | AAGATAGGCT | AACTGGCTTC |
| 13601 | CCCAACACCA | TGCAGGTAAT  | TAGTGATAAA | GGCAGGGTTG | GAACCAAAC  |
| 13651 | TGACCTCCCA | ATTGTGCTCT  | TAATGGCCAG | GACACTCTGT | GTCTTGAGCC |
| 13701 | ACACTTCCTC | CATGTTTTCT  | AGGGCTTTCT | AGGGAGGCAG | ACAGTGATGG |
| 13751 | GAAGGGGTGT | TCTTTAGTGT  | GGATGTGCCC | TGCCTGCTCC | TTTCTGTAAG |
| 13801 | CGTCACAGCA | CCTCCACTGC  | TGTACTGGGG | AGGCACCAAG | TTTTTCCCTG |
| 13851 | TTTGCCCAAC | CAAGGCGAGC  | TAGCTTAGGA | GTCACGTGAG | TGCTGGGTGT |
| 13901 | CTCGCCTGCT | GCATCCCTCT  | ATCCTGCCCC | TGCCCCCGGT | GCCCAGAGGA |
| 13951 | GGGCCCTGCC | TGTCTTCCCA  | GTTCTCCAAC | AGCAGCGCTG | TCCCAGCACC |
| 14001 | CTCGGGCTCC | AGTTGTGGCC  | TGGCAGCTGC | TGGGGCAGAC | ACCATACAGA |
| 14051 | CAGAGTCACA | GCAGGAAGAG  | GATGGGGCCC | AGGGCTGCTG | CCTCAGGCCA |
| 14101 | TGGCTGCATG | GCACCATCAG  | TTGATTGAGG | AGCTTTTCTT | GCCAATGTCT |
| 14151 | GAGGCATCAG | GTGGCAGGAC  | ACGTCTCCCT | GCTCTTAAGC | CTCAGGCATG |
| 14201 | CAGCCCTTCT | TATGCTCTCT  | GGGGTGAGGG | GGAGATCCCC | CTCATGGAAT |
| 14251 | TGCTTTTTTT | TTTTTTTTTT  | TTTTTTTGAG | ACAGGGTCCT | GCTCTGTCAC |
| 14301 | TCAGGCTGGA | GTGCAGCCTC  | AACCTCCCAG | ACTCAAGTGA | TCCTCCTGCC |
| 14351 | TCAGCCTCCC | GAGTAGCTGG  | GACCACAGGT | GGACACCATC | ACACCTGGGT |
| 14401 | TTTTTTGT   | TTTGTTTTTT  | GTTTTCTAGA | GATGGGGTCT | CACTTCTTGT |
| 14451 | CTCAGTCTGG | TCTCGAATC   | CTGGGCGCAA | GCAGTCTCTC | CACCTCGTCT |
| 14501 | TCCCAAAGTG | TTTGGATTAC  | AGGTGTGAGC | CACTGTGCTT | GGCCTTTTTA |
| 14551 | TTTATTTAGA | ATTTGTTTTG  | GAATTGCTTC | TTTATGCCTG | GCATATGCT  |
| 14601 | GGCACTATGT | GGCAGAGATT  | TTAAAAACGA | GCAAACAAAA | CAAATGCTTT |
| 14651 | GTCAACCACA | AAATGTATTC  | TCTGCCCCCT | AGGTCTTTTT | TGTGTAGTTG |
| 14701 | AGGCTAGAAG | ACAAAAATAG  | GGGGCAGTAA | GGAGCAGGGA | GCGATGTTTT |
| 14751 | AGGAGGTCTT | CCTTCCAGCC  | CCCTTGTTGA | AGCATCTGGC | TCACTAGCTT |
| 14801 | GGGGGAGCCA | TTAGGCAGCA  | GTGGCCAATC | CTGAGGCACT | CTCAGGTGTC |
| 14851 | ACTAAGAAAA | GGGGCATGTG  | CTCTATGGAT | ACCCATGGGC | TGAACCTGGA |
| 14901 | GTCTGGTCTG | GACCCATGGC  | TGTGCTAGGA | TCCACCGTCC | CCAGCCCCAA |
| 14951 | CTGCAGTCAG | CATGTTTCATC | ATCCTTAGGC | CTCTCCGCTT | CTTCTGTCAT |

FIGURE 3E



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15001 GTTTGTCTGC CTCATGCCCT GCTCATTACC AACTGGTCAG TCCCCACTGC
15051 CCTGCCTGGA GTGAGCTGGT TTGATTGGCT TAGCTAAGCT CCCTTGCCCTC
15101 TGCTGGCCAG GTCACCTGT GGGTCACCAG CAAACCTGTT GATGGTCCAG
15151 TCTGAACCTG CTTCTCCACA AAGAACATGT TGCACCCAGC CTTGCTTCTC
15201 TGAGCAGAGG TTTGGGGCTG AGCTGTTCTA GCCAGAAAGG GACACAGGGT
15251 GTGGCAGGCA CCATGATGGG CATATCTAAT GTGCCGGGAA AAACAATGAG
15301 CTGCTCTCCG TGCTTTGGGC ACCTGGTTGG GAGAGGGCCC ATCTGTCTGA
15351 CTTTCTCCTC CTGGGGCTCT CAGCGTCTCC GAGAACCTCT GCCAGAGCTG
15401 TGTAGAAGTG GTTTGCTTGT TTCTTAACAC TTCTGTGCCC TATTTCTTTC
15451 TGTACCCAAG AAAGGAAGTA GACTGTTTGT TAGGGACACT GTCGGGGTGA
15501 TGAATCTGGA CTTACTGGAA TCATGAACCA TGCCAAGGAG GAAGGAGAAA
15551 ATAGGCTATG GTGGGTGTCT TAGTTAGGGC TGGCTGCTGT AACAAAATGC
15601 CTTTAGCTGA CTAATTAAAG GCAAGAGAAA TGTATTGCTC AGAGTTGGG
15651 AGGCTGGGAA GTCCAAGATC AGGGTGCCAG CAGATTCAGT GTCTGGTGAA
15701 GGCTGATGCT CTGTGACAAA GGTGGCACCT TCTAGTCCA TCCTCACATG
15751 GCAGAAAGAG GAACAAGCTC CCTCAGACCT CTTTCTAAG GCGGTTAGTC
15801 CCATGCATGA GGGCTCTAAC ATCAGACTG AGTCACCTCC CAAAGCCCTC
15851 ACCTCCACC AGCACTGCAC TGGGGATTAA GTTCAATAT GGAATTTTG
15901 GAGGAACACA GACCTCAGA CCACAGCAGC GGGCTTCTCC TCATGTGCCC
15951 CCTGCCTCAC TTCTAGATGC CGCATAATGT CAGTGAACC CCGTCTCTAC
16001 TAAAAATACA AAAAATTAGC TGGGTGTGGT GGCACGTGCC TGTAATCCCA
16051 GCTACTTGGG AGGCTGAGGC AGGAGAATCG CTTGAACCCA GGAGGAGAG
16101 GTTGCACTGA CCTGAGATCG TGCCACTGCA CTCCAGCCTG GCGACAGAG
16151 GAAGACTCCG TCAAGAAAAA AGAGAAAAGG CATCAGGTAT GCCAGGGTGT
16201 GCGGAAAAAG GCATCGGGTA TGCCAGGGCG TGTGGGAAA GGCATCGGGT
16251 ATGCCAGGGT GTGTGGGAAA AGGCATCGGG TATGCCAGGG CATGTGGGAA
16301 AAGGTGGTAA GATTCTCAG CCTCCAGGG TTGGGAAGCC TCTGGCCGAG
16351 TGAAGCATAC CCTGGGTGGG TTTTAAGACA CCAGCTTCC AGTCCAGCTC
16401 AGCTGTGGGA TGTGGGAACA TGAGTCAGTG GGAACATGAG AATTGGCTTC
16451 CCTGTGGCTC ACAATAATAC CTACTCCTGC CTACTTCATG GGACCCGCAT
16501 AAGAGCTGAG GGATTCCATA GCTCAGGGGT ATGCTGTAAA GACAAGCACT
16551 ATGCACCTGG GTGTGGTTCT GAAACTTTCT TGTGCAGAAG AGTGAGTAGG
16601 GCTGGGCGAG TCCTGAGAAT GTGCATTCT CACACACCTC TGATGCTGCT
16651 GATGCTCTAG TCCCTTGCT GGCAAGGGTA CCTGGTTAGT AGGGGCCAGG
16701 ACTCTGTAAT GCCTTCCACT TCAGGGTTCT CTGGGCTGGT TTTCTGACT
16751 CCCCAGGAAG CCTTTATTCA GCAGAGGGAA GGTAGGAGTG AGAGGACTAC
16801 GCTGTCACTG CTTACATAC ATCGTTTAAT TTATCCAGC ACAGCCCTTA
16851 GGAGGGAAGC AGTATTCTCC TTCTACACTT AAGAAAATCG GCCTGGTGCG
16901 GAGGCTCATG CCTATAATCC CAGCACTGTG GGAAGCTGAG GCGGGAGGAT
16951 CGCTGGAGCC CAGGAGTTCA AGACTAGTCT AGGCAATACA GGGAGACCTC
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17051 AGTCCCAGCT ACCTACCCAG AGGCTGAGCT GGGAGGATTG CTTGAGTCTT
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17151 TGGCAACAGA GTGAGACTCC ATCCCAAAAA AAAAAAAAAA TTGAAGCTAG
17201 GAGAAGTTGA GACTTGCCCTG AAGTTACACA GTAAGTGCCA GAACCAGGAC
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17501 GTGCTCTCGC TCTCTTGACA CTTCAGGTGC AAAACTTTTG TCCTAATGTC
17551 GTTCTCAAAC TTACGCATGT GTGAGAATCA CTGTGAGAGC TTATTGAAAC
17601 TGATTGCGGG ACCCATACC TAGAGGGCCT GATTCTATAG GTCTGAGGTA
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17801 GATTCTCCCC ACACCCAGCA CCCGCTCCTG AGTAGCTGGG ATTACAGGTG
17851 CCCGCCACCA TGACTAGCTA ACGTTTGTAT TTTTAGTAGA GACGGGGGTT
17901 TCACCATGTT GGCCAGGCTG GTCTCAAACCT CCTGACCTCA GGTGATCCAC
17951 TCACCTCAGC CTCCAAGGT CTTGGGATTA CTGGTGTGAG CCACCGCGTG
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FIGURE 3F



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18001 CGGCCAGAAT TTGCATTTCT AACAGTCCC AGGTGATGCT GATGCTGTGG
18051 GTCCAGGGAC ACACTTTGTAG AACAGCTTGT TACTCAGGCG ATATGTGGAC
18101 AGTAGCGTCA TCTTCACCTG GGAGCTTCCT GCAGCATCTC AGGCCTTGCC
18151 CTACACCTAC CAGATCAGAA TCTGCATTTT AACTCAATCC CCGCGTGATT
18201 CTCATGCACC TGGAAGTTTG AGAAATATGA CCTTAGAGGA GCCGGAATGT
18251 GAAACCACTG GAGGCAGAGA TAGATGGAGA ATATCTCTTC TTCTCACGGA
18301 TACTAAAGAT GCAACAAAAA GGGCTGACTC TCTGGGTGTG CACCCAGGTG
18351 GGGCTGATGA CCGAAAAGAG GCCAGATGTG GACAGAGGAC TCTTCCCTGA
18401 GGGAAAGGCAG AGAGAACTTA GGAAAATCTG AAGAAAGGAG GTGGCTTCAG
18451 AGGAAAGGCA TTCATCTGGG CCATAAAACA GTGGAGAAGG TATCCTGCTG
18501 AGAGCACAGG GGTGGGGAGG GGGTGCCCTG GAGCTGAAGT CTTAGTGGG
18551 GGGACAGTGA TAGGTGAACA CACATGTGAA TAAACAGTTT GCTAAGCAGC
18601 TGCGAGGGCT GGCCAAGGTG AGAAAGCATC CGTCTGCAGA GGCTCAATA
18651 AGGCCAGTGT GTTGACTTTG TCCTGCAGTG CTCAGCAGTG GAAAAACCA
18701 ACAGCCACGC AGGGAGAGGG AAGGAGCCAC GATGGGCACG GGTTACTGGG
18751 GCCAGGGCTT GACTGGTAGG TGGACACAGC TGAAGGCCCA GGTTGTGTGG
18801 GAACAGAGCG CAGAAGCAAT AGATTCCCTCT TGAAGATCCT TGGGCTGTTA
18851 ACCTTTTFTA AATTTAAGAG AGGTTGTGTG GGCGGGGAGG GAGGAAGGAA
18901 AATCCTTTCAG AATCATAGA CTTACTCTGT TTCTTCCATC ATATGTGAAT
18951 GCATATGAAT AGCCAAAAGG TGAATAAAAC ACATGTTCCC AGGTGGCCAG
19001 TGAGACCTAG GTTGCAAGAT GGTGGGGTGT GTGTGAGGCC GGGGAGTGCT
19051 GCGAGCCCGG GAATTCCTCA GCCTTAGTCC CCCGCCACAT AGCTAAGAAG
19101 TGAGGGAGGA GGTGAGAAGG AGTCACTGCC CAGCCTCACT TCCGGTGGAG
19151 TACCCTGTCT CTTGTTCAGT TCTGTCTCTG GGGACAGTTG CTTGCTTTCA
19201 CCTCTCCCTC CATCCCTCTT TCTCTCACAG GGAAAATTC ACCTTAATAT
19251 TGGAAGTTCC TCTCCTAGCA AAGTCCTTCT CAGGCACCCA CAGGCAAAAA
19301 GGAAACTAAG CAGAGTTAGG GCTTCCAGGC CTAGCCAACT ACACGACTCT
19351 CCTCTTGCTT CCCTAAGAAC CAGCGCAAGG GGCAGCGTGG GTTCCAGCAT
19401 AGATGGACCT GTGTTGGAAT CTCTGCACGT GCTGTGCTGA CCCTGGCTAG
19451 CCATTGACCT CTCTGAGCCC TTGTTTCCTT TCCACTAGGC TCTCTGAGGG
19501 CAGGGGCCAT GTCTTTTTC A CTGCTCTGTC TGCCTGAGC ACTGTGCAGG
19551 GCACATAGGA AGTTCCCAT AATGTTTGTG GGATAAAGGA AATAAAACCT
19601 TCTCTCTTCC TGTCCCCCTT GTGATGGCTT TGCACAAGGC ACTGTCCTTG
19651 GCCAGGTTTG CTAGGCTAGT GTGAGGATAA ACCAGGTATA TTACAAATTG
19701 GAGAAAAATT CTCGTCTCTC TTGGAAGAAG GTGCTGTATC ATGAAACAAG
19751 AATGCTTTGA TTCCCTTCTA TGCCAGGTAC TGGGGAGAAA CAGGTGCCTG
19801 ATAACCGTTG ATCCAGGCAG AAATAAGCAT ACTCCTGCTT CCCAAGGCCT
19851 GATGCTTCTC TCCTTCCCTC CTTCTCTCTT CTTCTCTCTT ACTCTTCTC
19901 TGCACACATG GAAGAATGGC TGCCAGGCAT TGCCCATTTG GAAAAGTACA
19951 GCTCAATGGA TATGAATCAG CTTGGGCAGG CGAGAAATGA TTCACGCTG
20001 ACCAAATCGA TTTAGTTCAG GTTGCCCGTT CTGCATCTTT TTTCCCTTGT
20051 AATTAAATGA TGATTGGTCT TGATGGTGGG AAGGAAGAGA CAGAATTAA
20101 TTTGTTTGCC TTTGTAGAAA GCTGGGGACA GCACAGATAA GGGAAGATGT
20151 CTCCCATTTG GCAAATAACT GATGCGGAGG TGGAGTGGCA GTGGTGATGG
20201 GGATGCTGGT GCCTTCAGGC CTTCTGGGCC GGGCAGTGCA GCTGGTGGCA
20251 GACGGTTCGG AACTCTACCA TGTTCCCATC TGAAAACGTG GGCTGATCAT
20301 GCCCACCTCT GACCTTGCTC CAGGGAGTAC ACAAAGACGT AAGCTTAATT
20351 AACCACACAG ACGTAGCTCT TGAATCCCTG GGCATAGTGC CTGGGTATAG
20401 TTAGAGTTGG GGAGAGGCAT GGTGAGCAAA ACAACCTCCC TCATCTCTCT
20451 GTTGTCACATC AGAGTCAAGC TGGCTGCTGC TGGTGGTGCT GACTTCTCTT
20501 GCTGCAGATT TCTCCAATAT GTTCTGCCCC TGCACGCATT TGCCAAATCC
20551 CTTGCGTTTC TGTGCTCTCG TTGCGAGCTTA GCTCCTCCAG CCCTTGATG
20601 AAGAAGCGTG GGAACCTTTT GCTTCCCTTC CCTCCCGCAG TGACATGCCA
20651 TGCCATGCCA CTGCCTCTTC ATCTGGTCTT ATGACAGTCA CTCATAAGCA
20701 CCCGCATGTA CCCGGCCCTG CACTAGCTCA TGACAGCTGC AGTCAATTGG
20751 GCCAGGTGCT GTATCTCATC CGGCCTCCTC AGCAACCTC TGAGATACTG
20801 GTAATGTCCC TGATGAAGAT ATTTACTGAG GCAGAAATGG ACGCTCAGTG
20851 AAGCAAGGTG CCTGATGTTA TAGCAATGAG CTATGAGTGG CCAGAGGGAG
20901 GAGATAAGCT CAGGCCTGAC ACCAAAGCCC ATGCTCCTTC TAGTCAACCA
20951 CAGTGCCTCC TATGGTGAAT GAGTGAGTCA GCAACCAAGA CGCATGAGGC
```

FIGURE 3G



Docket No.: CL001188  
Serial No.: 09/817,198  
Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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```
21001 CTTCTTTTGTG GTGAGCCTTG GCTGGGTGCT GAGGCTTCAG GTACAATCAT
21051 GGGTTGGAAG AGCCCTCCTC TCTCTCCACA GTCTGGCACT ATGACCCCTT
21101 CTGGTTATTA ACAAGGCAAA GAGAGAGAGG GAAGAAAGCA GGCAAATAAT
21151 GTGGGTGCTT ATTCTAGAG ATTAGAATT CAGGAAGGAT AAACACAGCG
21201 TTCTCTCCAG AAGTATAAAT AGGAAGACTT CACACATGAC TAGAACGAGA
21251 CATGTTTTAA GTCTGTGCGAG TAAGGCAGTG ATGAAGTAGA TTTCCCCAGA
21301 TTCCTCTCC CTCTCTGGG TCCCCAGGG CCTTTACTTG TGGCAACTTT
21351 CAGCTCAGGG AGGGAGGAAA GCCCCTTTCA AAGCTTCAGA TACTTCCTTA
21401 AGGTCAGTTT CTGCTTAAAG AAGGCCTTCA CATTACTTCA TCCCTTTGCC
21451 AAATTAAACT GAAAGGAAAC CTTTCAAGTG TGATTGCGCTG GCCCTTTCCCT
21501 GTTCATTTCT CGTGGGTACG CTTTCTAACT TTCTTTCTTT CTTCCTTTCT
21551 TCAGGTGTTG ACTTTAAGAT GAAGACCATA GAGGTAGACG GCATCAAAGT
21601 GCGGATGATC ATCTGGTGAG CTGGGGAGGA GGAGGAGGCA GATGTAGGAG
21651 AAGAGGACTT CTGGCTGCTC CTTAGCTGCC CCTGCCATGT GTAAAATTCC
21701 TAGGCTTCAC CTGGGATAAC TGGCCACCTC TCTGATGGAT GGAAGCGAAG
21751 TCTCAGAAGC CCATCTCTTC CTATAAGCCT TAATCTCCAA CCTCTAAGAA
21801 ACTTTAGGGG ATTGACTACA AGCACCAAAG GGCAGGAATT AGAAGGAAGT
21851 GGCACACTAA CCATTGTGAA TTTATCTCAG GATTAGGCTT TGCCCTTGGG
21901 CTGTGCTTAA CTATTGAAG ATTGGAAGGA AGGAGGCTAC ACCCCCCATC
21951 ATTTAGGGCG AGACCTTGAG AGAGTTCCTC AGGATAGCAT GATGAAGTTT
22001 CCACAGTAGC AGAGGGTGCT GCTGTGGCTC TCTGCCTGAG GTCTTGGAAG
22051 CACTGCCTTT GCCAGGTTT AGAGCTCCCT CTCAATTCCA CAGCAGTATG
22101 GGCCTGCCT TCAGAGGTCC CATAGGACT AGGGGTGTAG CAGCATCCCC
22151 TGCCAACCTCC CATCCAACCA AATCTGGCCA CAGTGGCCAG ATTCAGAGA
22201 GCTGTCCAAG GCCTGTCTG GCTGTGGCTT CTGGTTTCTG CCAGGAGGGC
22251 AGTTGGCAGG AGGGGCCAAG GCCCTGCAGG CCTGGTCAGC ACCAGCACAG
22301 ATGACCAGGC CTCTGACTGC AGATCCCTGT GGGGATCCAA GCATCCCTGG
22351 TTTTTCACCC TTTAGCTCCC CAGTTTTTCC TACAAGGGGA CAGCTCTGCT
22401 CTTCCCTCC CCGTCTGTTC CCATGGTCCC TGCTCCTCTG AGGGACTGGC
22451 TTTCTCCTGC AGGGACACTG CAGGGCAGGA GAGATACCAG ACCATCACAA
22501 AGCAGTACTA TCGGCGGGCC CAGGTAAGCC ACCACATTGG GGGTTTCAA
22551 GTGGGAAGCT GCCACCCACA CTCCAGCTC TGGGTATTG AGATGTCTGT
22601 GCCACGGATC CCCTAAATAC AGTTCGCCTG CTTGGAGGAG CGCAGGGCGT
22651 CTTTCAGCTG TTTACTGATC ATTTGTCCGT CCATTGTTCA TGGCCCACTC
22701 ACTGCAGGCA GGCCCTGCC CTCACCCCTG ACTTCCACCC TCCATCCTGG
22751 GTCAAAGATC CAGGTCAAAG CATGTGGTGT CTTCTCTCTG TAGAGAGTTC
22801 TGTGATGGGC CTGGGAGGCG GCAGTGGTGG GGTCTGAGAG AAGAGATATT
22851 TCTGGATGCT GAGCAGGAG AATGGGAGAG TGGGACCAA CCTTTAAGTT
22901 TCCACGGCCC CTTCTGGCCC CATGACTGCA CTCTCTCTGT GCATATCACA
22951 TCTCTCTATT TCTCTCTCTC TCAGGGGATA TTTTGTGTCT ATGACATTAG
23001 CAGCGAGCGC TCTTACCAGC ACATCATGAA GTGGGTGAGT GACGTGGATG
23051 AGGTAGGAGA TGCCACCTCA CTGCCGGGGT GTGGAGAGGG TGCCTCACCG
23101 GGAAGGCAA GGCGAGGGCC AGATGGGAAG GCAAATGCTT CCAGGAAGCT
23151 TTGCCTTCCA CAGCCCTGGA TGAAGACCTC TGGGTGAGTA AGACATGGGG
23201 AAGAAACCGA AGTGCCATG CCCTCACTCT CTATACCCTG CCAGGCCTCC
23251 ACGGCTGTGT CTTTCCCGA AATGAATTAG TTCCAAGTCT TCCCTGTGAG
23301 CAGCTTCTTT CCTGAAATCT TGGGACCAGG TGGAGTTGCA AGATTGGGAT
23351 CTAGTCTGG CTCTGCACAA TAGCTGTGGA GCCTTGGGAA GCCATTTGAA
23401 TCCTCTGGGT CCCAGTTCC TGTAAGATGA GGGCTGGACT TACATCCAAT
23451 GTCCTTTCCA GCTCTGATAC CAGTGGTCTA ACCCAAGGAA GCACAGTCT
23501 TAGCCAGAGT GTCTTCTACC CTAAGCTCTC CCCGTGATAC CCTTGAGGTC
23551 AGCCATGGCA CTTGGGGAG CCTGGCACCT GCATCCAGTC GGCCACCCT
23601 GTCCCTAGGG CTCTGGAATT GGTGGTGGC TGGAGGAGT GCAGACTCTG
23651 TAGGGAATAT TGGGGGGGCA GGCAGCACTC ACTGGCTGTT CTGCCCATCC
23701 TTTGTCCCTA GTACGCACCA GAAGGCGTCC AGAAGATCCT TATTGGGAAT
23751 AAGGCTGATG AGGAGCAGAA ACGGCAGGTG GGAAGAGAGC AAGGGCAGCA
23801 GGTAAGTGGA GGGAAAAGGC AAGTCCACCC CAGGTCTCTCT GCTGGGCCCTC
23851 CAGGGCCAGT CCTGAGCGTG GGGACCTAGG GGTGTGTTCC CCAGTGGCAG
23901 GTCCTCCAC ACGTCCCCAG CACCCCAAGG CCCTGGGGGA GTGGCCATCC
23951 TCGGAAGGCT TGTTGTCTGG GTTTCAGGAC AGAAGCCAG AGATTGGGG
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FIGURE 3H



Docket No.: CL001188  
Serial No.: 09/817,198  
Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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|       |            |             |            |            |             |
|-------|------------|-------------|------------|------------|-------------|
| 24001 | TCCATCCAGA | AACAAAGACG  | TCATAGGCAG | CAACTCTCCC | AAGTCCAGGT  |
| 24051 | CCCCAAATGC | AGGATTGCCC  | TCTGCTTAAG | AGATCATCCC | CGTGTTAGTA  |
| 24101 | ATGAAGGACT | TCAAGTTGTC  | AACCTCTTCT | CTGACAGCAT | CCAGGCCTAG  |
| 24151 | CTGCCATGTT | ACGGTCGAGA  | AATGATCTCC | CATCCCACCC | AACACTCCCC  |
| 24201 | CACTCCTGTC | CTTCTTACCC  | AGGAAAGAGC | CAGGGAGGCA | AATGAGGAGA  |
| 24251 | CAAAGAGCCA | CAGCTGGAGA  | AGCCATGGGG | GCAGAAAGGG | TAGGAGGATG  |
| 24301 | ACGCTGAGGG | AATGTCCAAG  | CATGCAGGGA | GACCATCCTC | CCAGAGAGCA  |
| 24351 | GAAAGAAATA | TTGGTTATTT  | TTTTTTTCTT | TCTTTCTTTT | TTTTTTTTTTT |
| 24401 | TTTGAGATGG | AGTCTCGCTC  | TGTCACCCAG | GCTAGAGTGC | AGTGGCGCCA  |
| 24451 | TCTCGGCTCA | CTGCAACCTC  | TGCCTCCTGA | GTTCAAGCAA | TTCTTCTGCC  |
| 24501 | TCAGCCTCCC | AAGTAGCTGA  | GATTACAGGT | GCATGCCACC | ACGCCTGGCT  |
| 24551 | AATTTTTTTG | TATTTTTAGT  | AGAGATGGGG | TTTTGCCATA | TTGGCCAGGC  |
| 24601 | CGGTCTCGAA | CAGCTAACCT  | CAGGTGATCC | ACCTGCCTCA | GTCTCCCAAA  |
| 24651 | GTGCTGGGAT | TACAGGCGTG  | AGCCACTGTG | CCCAGCCAAG | ATTGGTATTT  |
| 24701 | CTGAGATAAG | TTATCCACTC  | AGTCCGTGGA | CCTCAAGAGT | TTTCCTCTCC  |
| 24751 | CTTTTCAGTC | AATAGCGTTC  | CATTAGTACT | TAAAAAGAAA | TTGATTGTTT  |
| 24801 | GGTATAAAAT | ATAAGACATG  | GTCATTGACC | AATTTGAAAG | TAGAGGCAAA  |
| 24851 | GCCTACTAGG | ATAGTATTTA  | TTGAGCACTC | TATGTGTGGC | ACTGTGCTAA  |
| 24901 | GGCAAGCGCT | TTTAAGTGCA  | CGACCCCACT | GAATCATCCC | ACAACCATGG  |
| 24951 | ATGGGAGACA | CACTCAGTCT  | CCTTTAACAG | AAGATAAAGC | TGGGGCTTAC  |
| 25001 | AGAGAATGTA | CAACTTGTC   | AAGGTCACAC | AGCTAGCCAT | CAGTGGCAGT  |
| 25051 | GCTGCTATTC | AGGTCTGGGA  | CTGTGGGACT | CCAGAGCCCA | TGTTTTTTAC  |
| 25101 | GAGGATGCCA | TACTGCCACA  | ATGGATGGTG | TCTTTATCTC | CTGATATATG  |
| 25151 | ATTGTGTGTT | GGGAGGCGTG  | GGGTGGCAGC | TGGAAGAATG | GAGAGGCATA  |
| 25201 | TTTGTGGAGG | ATCTTCCCCC  | ATTCTCTGCT | ACCTCTCTTT | GGAGCTCCCA  |
| 25251 | GTCCCATCTG | AGAAATTATC  | TACTCTGAGA | AATCGTCACA | ACACAGCATG  |
| 25301 | GTTGTGAGTG | CAGTGGCAGA  | AGCCTGTGCC | TGGTTGTATG | GGCCCCTCCC  |
| 25351 | CTGCCTTACT | GACTCTCTTT  | CAGAAATGTC | CTTCTCTTGC | AGCTGGCGAA  |
| 25401 | GGAGTATGGC | ATGGACTTCT  | ATGAAACAAG | TGCCTGCACC | AACCTCAACA  |
| 25451 | TTAAAGAGGT | GAGAGCCCTG  | GTGACCAGGC | GCCCGCTCTC | TCGGGCTGAG  |
| 25501 | TCCAGCAGAG | GTGGGAGGAG  | GAGCCATAAG | ATGGACCTTA | TCCCTCAGGC  |
| 25551 | CGCTGCAGGG | TTGCCAGGGG  | AGAGGAGGAG | ACACTGGACT | AACCTGTGCC  |
| 25601 | CTTTGGTTTC | CAGTCATTCA  | CGCGTCTGAC | AGAGCTGGTG | CTGCAGGCCC  |
| 25651 | ATAGGAAGGA | GCTGGAAGGC  | CTCCGGATGC | GTGCCAGCAA | TGAGTTGGCA  |
| 25701 | CTGGCAGAGC | TGGAGGAGGA  | GGAGGGCAAA | CCCGAGGGCC | CAGCGAACTC  |
| 25751 | TTCGAAAACC | TGCTGGTGCT  | GAGTCCTGTG | TGGGGCACCC | CACACGACAC  |
| 25801 | CCCTCTTCCC | TCAGGAGGCC  | CGTGGGCAGA | CAGGGGAGCC | GGGGCTTTGC  |
| 25851 | CCTGCTGCTG | TCCTCTCGTG  | TGATGACCCT | ATTGAGTATC | AGTAGCCACT  |
| 25901 | ACTCCCCCTG | CCTGGCCCTG  | AGAGCGGCTG | TGCTGTCATC | TCAAGCAGCC  |
| 25951 | CCTGTCCCCA | GCCCCGTCCAC | CCTGGAGTGG | TCTTCTTCAG | CCTGTTTCCC  |
| 26001 | CAGCCACAGG | CCTGCTACGA  | CCCCCACGAT | GTGCCGCAAG | CACTGTCTCA  |
| 26051 | CCATCCCGCA | CCCACCAGAC  | AACAGCCAGG | GCTGGAGTCC | AGGCCACTTT  |
| 26101 | CAGCTGCTCC | TTTCTCCGTG  | CATCGTGTCT | CTTCTCTGCT | TTTTCTCTCT  |
| 26151 | TCCCCCACTT | CTCTTTCTCT  | GACCCCTCCC | CTCCGGTGCG | TTTCGTATCA  |
| 26201 | AAGCTCCTCA | AACCCCGTCC  | CCCGTGTGTC | CTGCTGTGTG | CAGCTCGCTC  |
| 26251 | TTTCTTTTCT | TCCTAAGCTA  | TCCAAGGGGA | TGGACCCAGG | CTCGTGGGGA  |
| 26301 | GGTTCCACCC | TTGGATCCAG  | GAAGAACCCT | CCACCCTGCC | TCGTGGGTGG  |
| 26351 | GCCAAAGGCT | ACAGGGTGCT  | TCTTCTCTTT | CCCCCACCCC | CACTGTCCCT  |
| 26401 | CATGTGCCAT | GGGCCTGCCT  | CCCCAGTGAC | CTGCGAAAGT | GGAGCATCGA  |
| 26451 | GGTAGGAGGG | AAACGGCAAC  | CAGGGAGTCC | TCGAGCCTGG | GGCTGCCCTA  |
| 26501 | CCTCTACCCA | TTCCCCGACC  | AGAGCTTTGC | CCTTGCTTGG | CTGCCCCGCT  |
| 26551 | GCCTCTTTGG | GGAAGTGAGC  | TCAGAGGCAG | GTGCTTCAGA | GAAGGAAACA  |
| 26601 | AAATGAGGGG | TGGCAGGGAT  | AAAAAGTCAC | CTCCATTCTC | TACCTCCCAT  |
| 26651 | GCAGCATGAA | CACAATTCTT  | CTCCACCTGG | CTCCCAAATT | TAAAGATGTG  |
| 26701 | GACCAAGGCC | TGTGGGTACT  | CCAGGGGCAA | GGAGAGCCCT | GGGGTCAGTG  |
| 26751 | ACACTGTGAG | GCCAACCATG  | CACTCCACAA | AGGGGAGCAT | TTGGAATGA   |
| 26801 | AGGACTAGCT | CCTATGTATC  | AGGTAAAGAG | CAAGGGAGAG | CTGGCCAGGG  |
| 26851 | ACAGCAGTTT | GCACAGCAGA  | GGGGAATGTA | GCAACAGCAG | GGCCTCCTAG  |
| 26901 | GCCCCATCTT | GCATTTCTTA  | GGTAAGAAGA | GCATTTCTCT | AGACTCCAG   |
| 26951 | GCGGAGGACT | GAGCCTAGCC  | TTCAGCAACC | AAGGTTCTCC | TGGGACCCAA  |

FIGURE 31



Docket No.: CL001188  
Serial No.: 09/817,198  
Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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27001 AGTTTATGGG AGAAGGGCAA AGACTTCATG GGAAGAGAGA AGGAAGGCCC
27051 TGGGTAGAAA CGCTTGGTGC TGTTCTCTTT GGCCTTTAAG ACAAAGCGCT
27101 CATCTTGCCC TCTACCTCCT GATAGGCTTG AGGGTTTGCC AACCACACTG
27151 TGGCTACAGG TGGAGGGAAG AGGACTCCTT CCTCCAGAGT GCTATGTTCA
27201 GGAAGTTTCT TTAACCCCAT ATGGCCCAAG AGTAGCTCGT AGGAGGCCCT
27251 TTAAAGACGG AACAAGTAAT TTACCAGTTC TACTGGGGTT CCTGCCACCC
27301 GTCCCAAGGT GGGCGAGGCC TAGGAAGAGG GTCATTCTTA AGCCACACAT
27351 TAGCTGCACT GCGTGGCTGC AGCCAAAACA AAGAACTGGG TGTTGAGTAT
27401 TCATCAACTA AGAACC AAAA TCCAGGGCAC TCATATGTGA AGGATAAGAA
27451 CCTCACTTCC TTACTCCTCC AAAAAGAAAGT GGGGAAAGAA CCATCAAACC
27501 TTTCTCTCTG ACTTACCAAA CCAGGAAAAC AGCAGGAGAG GGTGGCTCAG
27551 GACTTAGGGA CAGGGTATAG CTTAGATGGT GGAAAGCAAA GGAGAGCAGG
27601 AAGTTGTAAA TCATGGCTA ATGAGAAAAAG GAGACAGCTA ACTCTAGGAT
27651 GAAGCTGTGA CTAGGCTGGA GTTGCTTCCT TGAAGATGGG ACTCCTTGGG
27701 TATCAAGACC TATGCCACAT CACACTGGGG CTAGGGAAGT AGGTGATGCC
27751 AGCCCTCAAG TCTGTCTTCA GCCAGGGACT TGAGAAAGTTA TATTGGGCAG
27801 TGGCTCCAAT CTGTGGACCA GTATTTTCAGC TTTCCCTGAA GATCAGGCAG
27851 GGTGCCATTC ATTGTCTTTC TCTCCTAGCC CCCTCAGGAA AGAAGGACTA
27901 TATTTGTACT GTACCCTAGG GGTTCCTGGA GGGAAAACAT GGAATCAGGA
27951 TTCTATAGAC TGATAGGCCC TATCCACAAG GGCCATGACT GGGAAAAGGT
28001 ATGGGAGCAG AAGGAGAATT GGGATTTTAG GGTGCAGCTA CGCTCACCCCT
28051 AAACTTTTGG TGGCCTGGGG CATGTCTTGA GGCCCAGACT GTTAACCAGG
28101 CTCTGCTGGC CTGTTTACTC GTCACCACCT CTGCACCTGC TGTCTTGAGA
28151 CTCCATCCAG CCCCAGGCAC GCCACCTGCT CCTGAGCCTC CACTATCTCC
28201 CTGTGACGGG TGAACCTCGT GTAGTGTGTC TCGGGTCCAT ATATGAATTG
28251 TGAGCAGGGT TCATCTATTT TAAACACAGA TGTTTACAAA ATAAAGATTA
28301 TTTCAAACCA CCGGTGTGGC TGCCTGGATG AGTCCTTGGG GGTAGGTCTC
28351 ACTCAGACCC TGGCAGTGAT GTGGGAGGGA GAGAGGCAGT GCTGGTAGAA
28401 GCAGCTCCAG AAGCAAAGGC AACAGCAGTA GAGTGACCAC GGAAGCGGCA
28451 AACATTGTCT TCCCTTCTCT ACCTTCCCTA GTGCCACCTG CAGGGAGGCC
28501 CAAAGCAAAG CCCCGTTGCC CTGCATTGGG CTGGCACTGC AGAAATAAGA
28551 TGAAACACAG TTATCGAGAG GATGCTGAAC ATCTATGAGC AGGTTTTAAA
28601 GCCAAGATGA GTCTCATCTG TTTGTGTGGG TCAGGAACGG GTCTTCTGTA
28651 AGGCATGAGG TGGGACTGGA TAATCTTTCA GATTGTGTAT TGGATACCTC
28701 GGGGAGCAG AGGCAGACTG GGATCTCAGG ACTGCAGGTA TTTCATACTT
28751 TGGGATATGG AATTGATGGA (SEQ ID NO:3)
```

**FEATURES:**

Start: 2044  
Exon: 2044-2167  
Intron: 2168-21554  
Exon: 21555-21615  
Intron: 21616-22462  
Exon: 22463-22523  
Intron: 22524-22974  
Exon: 22975-23052  
Intron: 23053-23711  
Exon: 23712-23801  
Intron: 23802-25392  
Exon: 25393-25458  
Intron: 25459-25613  
Exon: 25614-25769  
Stop: 25770

**CHROMOSOME MAP POSITION:**  
Chromosome 14

FIGURE 3J



Docket No.: CL001188  
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Inventors: YE, Jane et al.  
Title: ISOLATED HUMAN RAS-LIKE PROTEINS...

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ALLELIC VARIANTS (SNPs):

| DNA      |       |       |                 |
|----------|-------|-------|-----------------|
| Position | Major | Minor | Domain          |
| 206      | -     | T     | Beyond ORF (5') |
| 4963     | C     | T     | Intron          |
| 8175     | G     | A     | Intron          |
| 10515    | T     | C     | Intron          |
| 13034    | T     | C     | Intron          |
| 13781    | T     | C     | Intron          |
| 14050    | A     | C     | Intron          |
| 14273    | -     | T     | Intron          |
| 17582    | T     | C     | Intron          |
| 17700    | C     | T     | Intron          |
| 18074    | T     | C A   | Intron          |
| 19328    | G     | T     | Intron          |
| 19570    | A     | G     | Intron          |
| 20892    | C     | T     | Intron          |
| 26465    | G     | A     | Beyond ORF (3') |
| 26472    | A     | G     | Beyond ORF (3') |
| 28071    | C     | T     | Beyond ORF (3') |
| 28096    | C     | G     | Beyond ORF (3') |
| 28403    | A     | G     | Beyond ORF (3') |
| 28467    | C     | G     | Beyond ORF (3') |

Context:

DNA

Position

206 GCTCAAGATTGCACAGCTGGTGAGTGGTGACACTGGGACTGGAACCCAAGTGTGCCTTAC  
TCCAGAGCCCTTGGCATGCACCTGAAACCCCATGTAAGCCCACCTGTGGAGACGCGCACCT  
CGAAATAATGGAATCCACTACATCAGTTCTCTTTAGCTTTCTGTGTAATCAGAGTAGCTAG  
CAGGCTCGGGATTTCGCCCCCGGC  
[-,T]  
TTTTTTTTTTTTTTTTTTGAGACAGAGTTTTGCTCTTGTTGCCCAGGCTGGAGTGCAAT  
GGCGCAATCTCGGCTCACCGCAACCTTCGCCTCTCAGGTTCAAGCAATTCTCCTGCCTCA  
GCCTCCCGAGTAGCTGGGATTACAGGCACCGGCCACCAGCCCAGCTAATTTTTTATAT  
TTTGTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACTTTTCCCTCTT  
ATTATAATTCAGACACTTAACCTGAAATATACCTTTTCAAATGAAGTAAATGGGCTTACC

(SEQ ID

NO:14)

4963 TATTAAGGGACTTGGGATTCTCCCTTATCTTGGGCGTGTTTTTCAGCATTAATAAACT  
TAAAGGAAAGAGTTGGATGGTCAAGAAAAGCTTTTTCCTTAAGTGATATGGACAGTTTCT  
CAAGGAGGTAGAAGGGGCAGCCAGGAGACAAATCAAGGAGCCAACGAAATGAGTGTAC  
AAGTCATAGTCATTGCTTATTTTTAAAAAATGCGTGTCTGTATGCCAGGCTCTGCACT  
GAGACCGAGAGATTCCAAGATGAATAATACCTACAGTCACTGTTCTCAAATTGTGCATTA  
[C,T]  
CTAAAAACACATTACATGACCATGTGCGCCACTGATCGAGGCACCTTTCCCAGGGGCTTTT  
TTTGTGAATTAAGAAAACAAGGTAATTCACCAAGTATTTGCAAGATAGTTGGCTTCTTG  
GCTCATGTGGATATCACCTAGGCCAGTACTTTTGTGATTTACTGTGTACTCCACTTTAAC  
GGCTGCGATCTTCTAGAGAAGAACCCGCCAGGGAGCAGTGAGAGGCCTCCCTGGTAGAC  
TGAGACACTGACTGTCCCTCCCCCTATCCTTTTCTGCTTTTCTGGCCAGCAGACCAGCAGG

(SEQ ID

NO:15)

8175 ATGCCAGGTGCCATGCTAAGATTTGGGGACACAGTGGTGACCAAAACAGACAGAAACCAA

FIGURE 3K





Docket No.: CL001188  
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Inventors: YE, Jane et al.  
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GGAGCTGGCTTACATTCCAAGGGAGTGCATAGGAAGCTGTGTTTCATTTCAGTTTCTGCT  
CTAGTACCCCCCTTTCCCTGGCAGTGCCAGGGTCTGAGAAGGAAGAGTGAGGTGGTGAGG  
AGGTGTGAAGCAGTGGGGTGACCTGAGAGGAGAGGATGGGGTGGCTTTGCCTCAAGGCTT  
GGGCCCTGCTAGGTGTGCTCTGCTCAGGCCTCTGTTTCTCCTCCTGACACAGGCACA  
[G, A]  
ACTCGGCCTCCCACCCCTTCCCCAAGGACATGACCTTGGAAGGAACATATCTGAAGCCC  
GCGGAGGGTTTCCGCTGCTGTGCATCTGTGCCACAGATCCGAGATGCACCCACAGCTGG  
GAGCACCGGTTCTCCCGCTACCTGCACTCCCTGGTTTCTGTTCTCTCCTCCTCCTCT  
TCCTTCTCCCCGCTCCCAGACAGGCTGGTGATGAGCTTTATAACATGAAAGCTGATATT  
TGGCCATTATCCTTCTACCCTGATTGCCAGCTCTTCTCAGAGTGCCTTCTTCTGTAATCC (SEQ ID  
NO:16)  
10515 CTGGTGAAGGCTTTGAAGAGGAAGTGACATTTGAGTGGAGTCTTGAAGACTAGGCAGGAT  
TCTCCAGGGGCCCTGGGTGTGGGGGAAGCACACATCCTCTTCCCTGTAGGAGGTGCTGTG  
GAGAACACCTCCAGTGGGGCTGCTACTCTTCAGCCTTGCTGGGGCCAGCTGGAGTGGCCA  
CACCATGGTCACACCAGCTGAAGTTCAAGAAGCCCCCTGCCAGGAGATTGCTTTGTGTGGC  
TCTGGGTGAGGGCAGGTGCATCTGGAAGCCCCCTTCTTCTAAGATGTTTGCTCCTGAGT  
[T, C]  
TCTATGTCCTAGTCTTTTCTTCCCTGAACCTTTTGCTACCAGTCAGCACAGCCCTGCCTG  
AGAAGGAGGCTGGAGGAGTGAGTGGTCAGTAGCCTGGTGGGTCTTGCTGCCTCTGTGGT  
GCCCCGTGGCCTAAGTAGCAGGCTTAGGGAGGCGAGACCCAGTTCAGGGGCTGCCAATG  
GGGAGCGAGATGGGTGGCTGGAGCACACTGCACATGTACCAAGGCTCTAGGGAGGTCT  
GTGCACAAGGCAGTGGGAAAAGCAAGGGGAAGACCCAGCCTGGTCAACATGGTGAAACCC (SEQ ID  
NO:17)  
13034 AGATTTGGGTGAGGACACAGCCAAACCATATCAGCTCCCGGATCCCTGTGTGAATGGGG  
TCTTTTTTGGTGTGTTGAGGGCTGCACAGGGTGACCTCTTTAGAGGTGACCTCCTGCCACA  
ACCCACAGGAGGTGCACATGGCCACACATGCTGGTTTCTGCACTGGGAGGGGCTGGGG  
CACTCCTGGGACCTGTGCTTGGTAACTGGAGCTGGCCTGGCCCTGGGGATTGGGTGTCTG  
CCTTGGGTTTTCAGGTGTATTAGGTTTCTCCTCGTTGTGGAGTCTCATTACTAATGAAAG  
[T, C]  
TCAGGTGCGACTGCTGGTCCTTTGGGCTGTGGTTGATCCTGGTGATAACATTTGGCACCC  
AGAGGCAGCCCTGTTTCCACTGAAGCATGCGGAGCTTGGCTGGCAGGCAGGCAAGCTGGC  
AGCTGCCCTTAACCCATGAGGTGCTGGCCCGCTAGTAGGCACACCCCTACCTGTGCCAGAA  
TTGAGGTTGTAGCCAGACTCCAGGAGCCATCTGGGCCCCACAGGGGGCGGCATTTCTCT  
TTTTGTTGAAACATTCCAGCCAAGTGCTGGCTTGGGCTTCATCTCTGTGCCACTCTCC (SEQ ID  
NO:18)  
13781 CCCTGTGTTATGGGTTTACACCTTATCTCACAATCTTAAAAAAAATTCTCTGAGAAT  
CCTCTGTACCCCCACTTTACAGGTGAGGAAACTGAGGCAAAGATAGGCTAACTGGCTTC  
CCCAACACCATGCAGGTAATTAGTGATAAAGGCAGGGTTGGAACCAAATTGACCTCCCA  
ATTGTGCTCTTAATGGCCAGGACACTCTGTGTCTTGAGCCACACTTCTCCATGTTTCT  
AGGGCTTTCTAGGGAGGCAGACAGTGATGGGAAGGGGTGTTCTTTAGTGTGGATGTGCCC  
[T, C]  
GCCTGCTCCTTTCTGTAAGCGTCACAGCACCTCCACTGCTGTACTGGGGAGGCACCAAGT  
TTTTCCCTGTTTGCCCAAGGCGAGCTAGCTTAGGAGTCACGTGAGTGCTGGGTGTC  
TCGCTGCTGCATCCCTCTATCCTGCCCCTGCCCCGGTGCCAGAGGAGGGCCCTGCCT  
GTCTCCCAAGTTCTCAACAGCAGCGCTGTCCAGCACCCCTCGGGCTCCAGTTGTGGCCT  
GGCAGCTGCTGGGGCAGACACCATACAGACAGAGTCACAGCAGGAAGAGGATGGGGCCCA (SEQ ID  
NO:19)  
14050 GGAAGGGGTGTTCTTTAGTGTGGATGTGCCCTGCCTGCTCCTTTCTGTAAGCGTCACAGC  
ACCTCCACTGCTGTACTGGGGAGGCACCAAGTTTTTCCCTGTTTGCCCAAGGCGAG  
CTAGCTTAGGAGTCACGTGAGTGCTGGGTGTCTCGCTGCTGCATCCCTCTATCCTGCC  
CTGCCCCCGGTGCCAGAGGAGGGCCCTGCCTGTCTTCCAGTTCTCAACAGCAGCGCT  
GTCCAGCACCCCTCGGGCTCCAGTTGTGGCCTGGCAGCTGCTGGGGCAGACACCATACAG  
[A, C]  
CAGAGTCACAGCAGGAAGAGGATGGGGCCAGGGCTGCTGCCTCAGGCCATGGCTGCATG  
GCACCATCAGTTGATTGAGGAGCTTTCTTGCCAATGTCTGAGGCATCAGGTGGCAGAC  
ACGTCTCCCTGCTCTTAAGCCTCAGGCATGCAGCCCTTCTTATGCTCTCTGGGGTGAGGG

FIGURE 3L



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APR 16 2003  
TECH CENTER 1600/2900

NO:20) GGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGGGTCCT  
GCTCTGTCACTCAGGCTGGAGTGCAGCCTCAACCTCCCAGACTCAAGTGATCCTCCTGCC (SEQ ID

14273 TCTCCAACAGCAGCGCTGTCCCAGCACCCCTCGGGCTCCAGTTGTGGCTGGCAGCTGCTG  
GGGCAGACACCATACAGACAGAGTACAGCAGGAAGAGGATGGGGCCAGGGCTGCTGCC  
TCAGGCCATGGCTGCATGGCACCATCAGTTGATTGAGGAGCTTTTCTTGCCAATGTCTGA  
GGCATCAGGTGGCAGGACACGTCTCCCTGCTCTTAAGCCTCAGGCATGCAGCCCTTCTTA  
TGCTCTCTGGGGTGAGGGGAGATCCCCCTCATGGAATTGCTTTTTTTTTTTTTTTTTTTT  
[- , T]  
TTTTTGAGACAGGGTCCTGCTCTGTCACTCAGGCTGGAGTGCAGCCTCAACCTCCCAGACT  
CAAGTGATCCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACCACAGGTGGACACCATCACA  
CCTGGGTTTTTTTTGTGTTTTTTGTTTTTCTAGAGATGGGGTCTCACTTTCTTGCTC  
AGTCTGGTCTCGAACTCCTGGGCGCAAGCAGTCTCCACCTCGTCTTCCCAAAGTGTTT  
GGATTACAGGTGTGAGCCACTGTGCTTGGCCTTTTATTATTAGAAATTGTTTTGGAA (SEQ ID

NO:21) 17582 GGATGTTTCTTCCATGACATATATAGCTCTTGAACTACTTCTATCTAATATACCCACA  
GTGCTGTTAAAAATACAGATTTCTGGGCCTCACCTCAAATTATGATTCAGTAGGTCTAG  
GCACGTCAAGGTCAATTGTTTTTGTCTTTGTTTTAAGTCACCCCAGGTGATTCTAAAGCCG  
AAGCTCTGCAAAGCACACCTTGAGAAACAGAGAACTCTTGCTCTCGCTCTCTTGACAC  
TTCAGGTGCAAACTTTTGTCTTAATGTCTGTTCTCAAACCTACGCATGTGTGAGAATCAC  
[T , C]  
GTGAGAGCTTATTGAACTGATTGCGGGACCCCATACCTAGAGGGCCTGATTCTATAGGT  
CTGAGGTAAGGCCCAAGAATTTGCATATTTGCATTTCTGTTTTCTTTCTTTCTTTCTTT  
TTTTTTTTTTTTTTGAGATGAAGTCTCACCTGTGCGCCAGACTGGAGTGCAGTGGCATGA  
TCTCAGCTCACTGCAGCCTCTGCCTCCTGGGTAAAGCGATTCTCCCCACACCCAGACC  
CGCTCCTGAGTAGCTGGGATTACAGGTGCCCGCCACCATGACTAGCTAACGTTTGTATTT (SEQ ID

NO:22) 17700 AGGCACGTCAAGGTCAATTGTTTTTGTCTTTGTTTTAAGTCACCCCAGGTGATTCTAAAGC  
CGAAGCTCTGCAAAGCACACCTTGAGAAACAGAGAACTCTTGCTCTCGCTCTCTTGAC  
ACTTCAGGTGCAAACTTTTGTCTTAATGTCTGTTCTCAAACCTACGCATGTGTGAGAATC  
ACTGTGAGAGCTTATTGAACTGATTGCGGGACCCCATACCTAGAGGGCCTGATTCTATA  
GGTCTGAGGTAAGGCCCAAGAATTTGCATATTTGCATTTCTGTTTTCTTTCTTTCTTTT  
[C , T]  
TTTTTTTTTTTTTTGAGATGAAGTCTCACCTGTGCGCCAGACTGGAGTGCAGTGGCAT  
GATCTCAGCTCACTGCAGCCTCTGCCTCCTGGGTAAAGCGATTCTCCCCACACCCAGAC  
CCCGTCTCTGAGTAGCTGGGATTACAGGTGCCCGCCACCATGACTAGCTAACGTTTGTAT  
TTTTAGTAGAGACGGGGTTTTCCCATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCA  
GGTGATCCACTCACCTCAGCCTCCCAAGGTCTTGGGATTACTGGTGTGAGCCACCGCGTG (SEQ ID

NO:23) 18074 TGCAGCCTCTGCCTCCTGGGTAAAGCGATTCTCCCCACACCCAGACCCGCTCCTGAGT  
AGCTGGGATTACAGGTGCCCGCCACCATGACTAGCTAACGTTTGTATTTTAGTAGAGAC  
GGGGGTTTCAACATGTTGGCCAGGCTGGTCTCAAACCTCCTGACCTCAGGTGATCCACTCA  
CCTCAGCCTCCCAAGGTCTTGGGATTACTGGTGTGAGCCACCGCGTGCGGCCAGAATTG  
CATTTCTAACAAGTCCAGGTGATGCTGATGCTGTGGGTCCAGGGACACACTTTGAGAAC  
[T , C , A]  
GCTTGTTACTCAGGCGATATGTGGACAGTAGCGTCATCTTACCTGGGAGCTTCTGCGAG  
CATCTCAGGCCTTGCCCTACACCTACCAGATCAGAATCTGCATTTTAACTCAATCCCCGC  
GTGATTCTCATGCACCTGGAAGTTTGAGAAATATGACCTTAGAGGAGCCGGAATGTGAAA  
CCACTGGAGGCAGAGATAGATGGAGAATATCTCTTCTCTCAGGATACTAAAGATGCAA  
CAAAAAGGGCTGACTCTCTGGGTGTGCACCCAGGTGGGGCTGATGACCGAAAAGAGGCCA (SEQ ID

NO:24) 19328 TGTGTGTGAGGCCGGGGAGTGCTGCGAGCCCCGGAATTCTCAGCCTTAGTCCCCCGCCA  
CATAGCTAAGAAGTGAGGGAGGAGGTGAGAAGGAGTCACTGCCAGCCTCACTTCCGGTG  
GAGTACCCTGTCTCTTGTCAAGTTCTGTCTCTGGGGACAGTTGCCCTGCTTTACCTCTCC  
CTCCATCCCCCTCTCTCTCACAGGGAAAAATTACCTTAATATTGGAAGTTCTCTCCTA

FIGURE 3M



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APR 16 2003  
TECH CENTER 1600/2900

GCAAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAACTAAGCAGAGTTAGGGCTTCCA  
[G, T]  
GCCTAGCCAACTACACGACTCTCCTCTTGCTTCCCTAAGAACCAGCGCAAGGGGCAGCGT  
GGGTTCCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCTGGCT  
AGCCATTGACCTCTCTGAGCCCTTGTTCCTTTCCACTAGGCTCTCTGAGGGCAGGGGCC  
ATGTCTTTTTCACTGCTCTGTCTGCACTGAGCACTGTGCAGGGCACATAGGAAGTTCCCA  
TAAATGTTTGTGGGATAAAGGAAATAAAACCTTCTCTCTTCTGTCCTTGTGATGGC (SEQ ID  
NO:25)  
19570  
AAAGTCCTTCTCAGGCACCCACAGGCAAAAAGGAACTAAGCAGAGTTAGGGCTTCCAGG  
CCTAGCCAACTACACGACTCTCCTCTTGCTTCCCTAAGAACCAGCGCAAGGGGCAGCGT  
GGTTCAGCATAGATGGACCTGTGTTGGAATCTCTGCACGTGCTGTGCTGACCTGGCT  
GCCATTGACCTCTCTGAGCCCTTGTTCCTTTCCACTAGGCTCTCTGAGGGCAGGGGCCA  
TGTCTTTTTCACTGCTCTGTCTGCACTGAGCACTGTGCAGGGCACATAGGAAGTTCCCAT  
[A, G]  
AATGTTTGTGGGATAAAGGAAATAAAACCTTCTCTCTTCTGTCCTTGTGATGGCTT  
TGACAAGGCACTGTCTTGGCCAGGTTTGCTAGGCTAGTGTGAGGATAAACAGGTATA  
TTACAAATTGGAGAAAATTTCTCGTTCTTCTTGGAGAAGGTGCTGTATCATGAAACAAG  
AATGCTTTGATTCCCTTCTATGCCAGGTACTGGGGAGAAAACAGGTGCTGATAACCGTTG  
ATCCAGGCAGAAATAAGCATACTCTGCTTCCCAAGGCCTGATGCTTCTCTCTTCTCTCC (SEQ ID  
NO:26)  
20892  
CCTTGGATGAAGAAGCGTGGGAACCTTTTGCTTCCCTTCCCTCCCGCAGTGACATGCCAT  
GCCATGCCACTGCCCTCTTCATCTGGTCCCTATGACAGTCACTCATAAGCACCCGCATGTAC  
CCGGCCCTGCACTAGCTCATGACAGCTGCAGTCAATTGGGCCAGGTGCTGTATCTCATCC  
GGCTCCTCAGCAACCCCTCTGAGATACTGGTAATGTCCCTGATGAAGATATTTACTGAGG  
CAGAAATGGACGCTCAGTGAAGCAAGGTGCCTGATGTTATAGCAATGAGCTATGAGTGGC  
[C, T]  
AGAGGGAGGAGATAAGCTCAGGCCTGACACCAAAGCCCATGCTCCTTCTAGTCAACCACA  
GTGCTCCTATGGTGAATGAGTGAGTCAGCAACCAAGACGCATGAGGCCTTCTTTTGGT  
GAGCCTTGGCTGGGTGCTGAGGCTTCAGGTACAATCATGGGTGGAAGAGCCCTCTCTC  
TCTCCACAGTCTGGCACTATGACCCTTCTGTTATTAACAAGGCAAAGAGAGAGAGGGA  
AGAAAGCAGGCAATAATGTGGTTGCTATTCTAGAGATTAGAATTTTCAGGAAGGATAA (SEQ ID  
NO:27)  
26465  
TTCTCTGACCCCTCCCTCCGGTGCCTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCG  
TGTGCTGCTGTGTGTCAGCTCGCTCTTTCCTTCCCTTCTAAGCTATCCAAGGGGATGGA  
CCAGGCTCGTGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTCGT  
GGGTGGGCTCAAAGGCTACAGGGTGCTTCTTCTCTTCCCCCACCCTGTCCTCATG  
TGCCATGGGCCTGCCCTCCCGAGTACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAAC  
[G, A]  
GCAACCAGGGAGTCTCTGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAGAGC  
TTTGCCCTTGCTTGCTGCCCGCCTGCCCTCTTTGGGGAAGTGAAGCTCAGAGGCAGGTGCT  
TCAGAGAAGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCT  
CCCATGCAGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCA  
AGGCTGTGGGTACTCCAGGGGCAAGGAGAGCCCTGGGGTCACTGACACTGTGAGGCCAA (SEQ ID  
NO:28)  
26472  
ACCCCTCCCTCCGGTGCCTTTTCGTATCAAAGCTCCTCAAACCCCGTCCCCCGTGTGTCC  
TGCTGTGTGTCAGCTCGCTCTTTCTCTTCTTCTAAGCTATCCAAGGGGATGGACCCAGGC  
TCGTGGGGAGGTTCCACCCTTGGATCCAGGAAGAACCCTCCACCCTGCCTCGTGGGTGGG  
CCAAAGGCTACAGGGTGCTTCTTCTCTTCCCCCACCCTGTCCTCATGTGCCATG  
GGCTGCTTCCCGAGTGACCTGCGAAAGTGGAGCATCGAGGTAGGAGGGAAACGGCAACC  
[A, G]  
GGGAGTCTCTGAGCCTGGGGCTGCCCTACCTCTACCCATTCCCCGACCAGAGCTTTGCC  
TTGCTTGCTGCCCCCTGCCCTCTTTGGGGAAGTGAAGCTCAGAGGCAGGTGCTTCAGAGA  
AGGAAACAAAATGAGGGGTGGCAGGGATAAAAAGTCACCTCCATTCTCTACCTCCCATGC  
AGCATGAACACAATTTCTCTCCACCTGGCTCCCAAATTTAAAGATGTGGACCAAGGCCTG  
TGGTACTCCAGGGGCAAGGAGAGCCCTGGGGTCACTGACACTGTGAGGCCAACCATGCA (SEQ ID  
NO:29)

FIGURE 3N



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28071 GCCAGGGACTTGAGAAGTTATATTGGGCAGTGGCTCCAATCTGTGGACCAGTATTTTCAGC  
TTTCCCTGAAGATCAGGCAGGGTGCCATTCATTGTCTTTCTCTCCTAGCCCCCTCAGGAA  
AGAAGGACTATATTTGTACTGTACCCTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGA  
TTCTATAGACTGATAGGCCCTATCCACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAG  
AAGGAGAATTGGGATTTTAGGGTGCAGCTACGCTCACCTAAACTTTTGGTGGCCTGGGG  
[C, T]  
ATGTCTTGAGGCCCAGACTGTTAACCAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTC  
TGCACCTGCTGTCTTGAGACTCCATCCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCC  
ACTATCTCCCTGTGACGGGTGAACCTCGTGTACTGTCTCGGGTCCATATATGAATTGT  
GAGCAGGGTTCATCTATTTTAAACACAGATGTTTACAAAATAAAGATTATTTCAAACCAC  
CGGTGTGGCTGCCTGGATGAGTCTTGGGGTAGGTCTCACTCAGACCCTGGCAGTGATG (SEQ ID  
NO:30)

28096 GGCAGTGGCTCCAATCTGTGGACCAGTATTTTCAGCTTTCCCTGAAGATCAGGCAGGGTGC  
CATTCAATTGTCTTTCTCTCCTAGCCCCCTCAGGAAAGAGGACTATATTTGTACTGTACC  
CTAGGGGTTCTGGAAGGGAAAACATGGAATCAGGATTCTATAGACTGATAGGCCCTATCC  
ACAAGGGCCATGACTGGGAAAAGGTATGGGAGCAGAAGGAGAATTGGGATTTTAGGGTGC  
AGCTACGCTCACCTAAACTTTTGGTGGCCTGGGGCATGTCTTGAGGCCCAGACTGTTAA  
[C, G]  
CAGGCTCTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACTCCAT  
CCAGCCCCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAAC  
TCGTGTACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACA  
CAGATGTTTACAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCT  
TGGGGTAGGTCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGT (SEQ ID  
NO:31)

28403 CTGCTGGCCTGTTTACTCGTCACCACCTCTGCACCTGCTGTCTTGAGACTCCATCCAGCC  
CCAGGCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACCTCGTGT  
ACTGTGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATG  
TTTACAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCTGGGGG  
TAGGTCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGTAGAAGC  
[A, G]  
GCTCCAGAAGCAAAGGCAACAGCAGTAGAGTGACCACGGAAGCGGCAAACATTGTCTTCC  
CTTCTCTACCTTCCCTAGTGCCACCTGCAGGGAGGCCCAAAGCAAAGCCCCGTTGCCCTG  
CATTGGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGATGCTGAACATC  
TATGAGCAGGTTTTAAAGCCAAGATGAGTCTCATCTGTTTGTGTGGGTCAGGAACGGGTC  
TTCTGAAGGCATGAGGTGGGACTGGATAATCTTTCAGATTTGTGATTGGATACCTCGGG (SEQ ID  
NO:32)

28467 GCACGCCACCTGCTCCTGAGCCTCCACTATCTCCCTGTGACGGGTGAACCTTCGTGTACTG  
TGTCTCGGGTCCATATATGAATTGTGAGCAGGGTTCATCTATTTTAAACACAGATGTTTA  
CAAAAATAAAGATTATTTCAAACCACCGGTGTGGCTGCCTGGATGAGTCCCTGGGGGTAGG  
TCTCACTCAGACCCTGGCAGTGATGTGGGAGGGAGAGAGGCAGTGCTGGTAGAAGCAGCT  
CCAGAAGCAAAGGCAACAGCAGTAGAGTGACCACGGAAGCGGCAAACATTGTCTTCCCTT  
[C, G]  
TCTACCTTCCCTAGTGCCACCTGCAGGGAGGCCCAAAGCAAAGCCCCGTTGCCCTGCATT  
GGGCTGGCACTGCAGAAATAAGATGAAACACAGTTATCGAGAGGATGCTGAACATCTATG  
AGCAGGTTTTAAAGCCAAGATGAGTCTCATCTGTTTGTGTGGGTCAGGAACGGGTCTTCC  
TGAAGGCATGAGGTGGGACTGGATAATCTTTCAGATTTGTGATTGGATACCTCGGGGGAG  
CAGAGGCAGACTGGGATCTCAGGACTGCAGGTATTTTCATACTTTGGGATATGGAATTGAT (SEQ ID  
NO:33)

FIGURE 30